

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:36:07 ; Search time 33:27 Seconds

(without alignments)
35.790 Million cell updates/sec

Title: US-09-489-760-5
Sequence: 4 VLRDDEA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4 25026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 4 25026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
SPTRMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rabbit:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*
```

Q9kiv3 streptomyces
Q9kf93 bacillus ha
P93619 vigna ungu
Q94249 chrysosplen
Q36681 quintinia v
Q9418 chrysosplen
Q9426 chrysosplen
Q78605 isotria ver
Q9416 chrysosplen
Q9kf93 bacillus ha
Q3148 saxifraga p
Q31822 antrophyum
Q31907 bolandra or
Q32207 elmera race
Q32484 jepsonia pa
Q33136 gullivertia
Q33509 hydrangea m
Q20245 achlys trip
Q9tln7 asteroptyrum
Q9qd7 quintinia v
Q9tfd7 tofieldia p
Q91v01 arabidopsis
Q06978 bacillus su
Q9w157 drosophila
Q86581 streptomyce
Q43088 schizosacch

ALIGNMENTS

Database : SPTRMBL_16:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Score Match Length DB ID Description

42 100.0 1165 4 Q92619 homo sapien

38 90.5 4150 2 Q9kiv3 streptomyces

36 85.7 174 5 Q9kf93 bacillus ha

35 83.3 616 1 Q27025 methanobact

34 81.0 238 14 Q9whx7 influenza a

34 81.0 239 14 Q9why9 influenza a

34 81.0 239 14 Q9why8 influenza a

34 81.0 239 14 Q9why7 influenza a

34 81.0 239 14 Q9why6 influenza a

34 81.0 239 14 Q9why5 influenza a

34 81.0 239 14 Q9why4 influenza a

34 81.0 239 14 Q9why3 influenza a

34 81.0 239 14 Q9why1 influenza a

34 81.0 239 14 Q9whx9 influenza a

34 81.0 252 14 Q9why2 influenza a

34 81.0 252 14 Q93188 influenza a

34 81.0 389 5 Q9xtd7 caenorhabdi

34 81.0 486 5 Q9ppu0 ureaplasma

34 81.0 791 5 Q9ng78 caenorhabdi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	42	Q9kiv3 streptomyces	42	100.0	1165	4	Q92619 homo sapien
2	38	Q9kf93 bacillus ha	38	90.5	4150	2	Q9kiv3 streptomyces
3	36	P93619 vigna ungu	36	85.7	174	5	Q9kf93 bacillus ha
4	35	Q94249 chrysosplen	35	83.3	616	1	Q27025 methanobact
5	34	Q36681 quintinia v	34	81.0	238	14	Q9whx7 influenza a
6	34	Q9418 chrysosplen	34	81.0	239	14	Q9why9 influenza a
7	34	Q9426 chrysosplen	34	81.0	239	14	Q9why8 influenza a
8	34	Q78605 isotria ver	34	81.0	239	14	Q9why7 influenza a
9	34	Q3148 saxifraga p	34	81.0	239	14	Q9why6 influenza a
10	34	Q31822 antrophyum	34	81.0	239	14	Q9why5 influenza a
11	34	Q31907 bolandra or	34	81.0	239	14	Q9why4 influenza a
12	34	Q32207 elmera race	34	81.0	239	14	Q9why3 influenza a
13	34	Q32484 jepsonia pa	34	81.0	239	14	Q9why1 influenza a
14	34	Q33136 gullivertia	34	81.0	239	14	Q9whx9 influenza a
15	34	Q33509 hydrangea m	34	81.0	252	14	Q9why2 influenza a
16	34	Q34148 saxifraga p	34	81.0	252	14	Q93188 influenza a
17	34	Q35059 hydrangea m	34	81.0	389	5	Q9xtd7 caenorhabdi
18	34	Q3509 hydrangea m	34	81.0	486	5	Q9ppu0 ureaplasma
19	34	Q36681 quintinia v	34	81.0	791	5	Q9ng78 caenorhabdi

RESULT 1
ID Q92619 PRELIMINARY;
ID Q92619; PRELIMINARY;
AC Q92619; PRELIMINARY;
DT 01-FEB-1997 (TREMBL); 02, Created
DT 01-FEB-1997 (TREMBL); 02, Last sequence update
DT 01-MAR-2001 (TREMBL); 16, Last annotation update
DE MYELOBLAST KIAA0223 (FRAGMENT).
GN KIAA0223
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW.
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nonura N.;
RA "Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA201-KIAA280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
RN [2]
RN SEQUENCE OF 170-1165 FROM N.A.
RP TISSUE=BONE MARROW.
RA Lamerind J.E., McCready P.M., Skowronski E., Adamson A.W., Ramirez M., Stilwagen S., Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S., Phan H., Velasco N., Garnes J., Dangathian L., Poundstone P., Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T., Christen M., Amico-Keller G., Cofield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O., Carrasco A.V.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; BAA13212.1; -.
DR EMBL; AAC04151; AAC03237.1; -.
DR HSSP; Q07960; 1RGP.
DR InterPro; IPR002198; -.
DR Pfam; PF00130; DAG_FE-bind; 1.
DR Pfam; PF00620; RhGMP; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.

DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 SMART; SM0324; RhogAP; 1.
 FT NON_TER 1 12734 MW; 92EF768CAFDF458C9 CRC64;
 SQ SEQUENCE 1165 AA; 12734 MW; 92EF768CAFDF458C9 CRC64;

Query Match 100 %; Score 42; DB 4; Length 1165;
 Best Local Similarity 100 %; Pred. No. 14;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VRDDLEA 9
 Db 166 VRDDLEA 174

RESULT 2
 Q9KIV4 PRELIMINARY; PRT; 4150 AA.
 AC Q9KIV4;
 ID Q9KIV4;
 AC Q9KIV4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE 8,8A-DEOXYLEANOLIDIE SYNTHASE 1.
 GN QLEA1.
 OS Streptomyces antibioticus
 OC Firmicutes; Actinobacteria; Actinomycetidae; Streptomyctaceae; Streptomyces.
 AC Actionomycetes; Streptomyces; Streptomyctaceae; Streptomyces.
 OC NCBI_TAXID=1890;
 OX RN
 RN RP
 SEQUENCE FROM N.A.
 RX MEDLINE=20163406; PubMed=10908114;
 RA Shah S., Xue O., Tang L., Carney J.R., Betlach M., McDaniel R.;
 RT "Cloning, Characterization, and Heterologous Expression of a
 RT Polyketide Synthase and P-450 Oxidase Involved in the Biosynthesis of
 RT the Antibiotic Oleandomycin,"
 RL J. Antibiot. 53:502-508 (2000).
 DR AF226951; AAFB8408; 1.
 DR InterPro; IPR00169; -.
 DR InterPro; IPR00255; -.
 DR InterPro; IPR00794; -.
 DR InterPro; IPR001227; -.
 DR InterPro; IPR002106; -.
 DR pfam; PF00109; ketoacyl-synt; 3.
 DR pfam; PF00550; pp-binding; 3.
 DR pfam; PF00698; Acyl transfer; 3.
 DR PROSITE; PS00339; AA-TRNA_LIGASE_II_2; UNKNOWN_1.
 DR PROSITE; PS50075; ACP_DOMAIN; 3.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
 DR PROSITE; PS00012; PHOSPHOPANTETHINE; 3.
 DR PROSITE; PS00639; THIOL_Protease_HIS; UNKNOWN_1.
 KW phosphopantethine; transpeptidase.
 SQ SEQUENCE 4150 AA; 43566 MW; 9383296C4C16647D CRC64;

Query Match 90.5%; Score 38; DB 2; Length 4150;
 Best Local Similarity 100 %; Pred. No. 3.2e+02;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LRDDLEA 9
 Db 1781 LRDDLEA 1788

RESULT 3
 Q94256 PRELIMINARY; PRT; 174 AA.
 AC Q94256;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE COSMLD_K04A8.
 GN K04A8_9; Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TAXID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Cooper J., Coulson A.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Craxton M., Dear S., Du Z., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Gardner A., Green P., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J.,
 RA Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Showkeen R.,
 RA Smaill N., Smith A., Sonnhammer E., Staden R., Sulston J., Watson A., Weinstock L., Waterston R.,
 RA Thierry-Mieg J., Thomas K., Vaughan K., Wohldman P.;
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."
 RL Nature 368:32-38 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Geisel C., Bradshaw H.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U61849; AAC48054; AAC48055; 1.
 DR InterPro; IPR000004; -.
 DR SMART; SM00118; SAPE; 1.
 DR SEQUENCE 174 AA; 19210 MW; A6303CF6383BEBD9 CRC64;

Query Match 85.7%; Score 36; DB 5; Length 174;
 Best Local Similarity 77.8%; Pred. No. 23;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLEA 9
 DR 1|:1|1|1|:
 Db 129 VLKDDLLDA 137

RESULT 4
 O2705; PRELIMINARY; PRT; 616 AA.
 ID O2705; PRELIMINARY; PRT; 616 AA.
 AC O2705; PRELIMINARY; PRT; 616 AA.
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE TYPE I RESTRICTION MODIFICATION ENZYME, SUBUNIT M.
 GN MTH042.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Buryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanothermobacter.
 OC NCBI_TAXID=142626;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DETA_H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., DeLonghery C., Lee H.-M., DuBois J.,
 RA Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabakar S.,
 RA McDougall S., Shiner G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.,
 RA RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics."
 RL J. Bacteriol. 179:1135-1155 (1997).
 DR EMBL; AE000868; AAC85440; 1.
 DR InterPro; IPR02052; -.
 DR InterPro; IPR02296; -.
 DR InterPro; IPR03356; -.
 DR Pfam; PF02384; N6_Mtase; 1.
 DR PRINTS; PRO0507; N12N6MTFASE.

DR PROSITE; PS00092; N6_MTA8P; UNKNOWN 1;
 SQ SEQUENCE 616 AA; 71715 MW; 064AF1076A5DBAD CRC64;

Query Match 83.3%; Score 35; DB 1; Length 616;
 Best Local Similarity 77.88; pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLREDDLEA 9
 ||| | | | | | |
 Db 465 VLREDDLEA 473

RESULT 5
 Q9WHX7 PRELIMINARY; PRT; 238 AA.
 ID Q9WHX7
 AC Q9WHX7
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 OS M.
 OS Influenza A virus (A/Taiwan/96/179).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
 NCBI_TaxID=94648;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/TAIWAN/96/179;
 RC Shih S.-R., Tsai H.-R., Chang S.-C.;
 RA "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 Taiwan." Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF138707; AAC3756.2; -.
 DR HSSP; P03485; IAA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR Prodrom; PD001061; -; 1.
 KW Matrix Protein.
 FT NON_TER 238 AA; 1 26266 MW; 401A494B5B673FOA CRC64;
 SQ SEQUENCE 238 AA; 1 26266 MW; 401A494B5B673FOA CRC64;

Query Match 81.0%; Score 34; DB 14; Length 238;
 Best Local Similarity 100.0%; pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLE 8
 ||| | | | | | | |
 Db 215 LRDDLE 221

RESULT 6
 Q9WHX9 PRELIMINARY; PRT; 239 AA.
 ID Q9WHX9
 AC Q9WHX9
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 OS M.
 OS Influenza A virus (A/Taiwan/98/346).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
 NCBI_TaxID=94660;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/TAIWAN/98/346;
 RC Shih S.-R., Tsai H.-R., Chang S.-C.;
 RA "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 Taiwan." Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RL AF138719; AAC3768.2; -.

DR HSSP; P03485; IAA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR Prodrom; PD001061; -; 1.
 KW Matrix Protein.
 FT NON_TER 239 AA; 1 26411 MW; 293533A39097E3E4 CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLE 8
 ||| | | | | | | |
 Db 216 LRDDLE 222

RESULT 8
 Q9WHY7 PRELIMINARY; PRT; 239 AA.
 ID Q9WHY7
 AC Q9WHY7
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 OS M.
 OS Influenza A virus (A/Taiwan/98/45).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A virus.
 NCBI_TaxID=94658;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/TAIWAN/98/45;
 RC Shih S.-R., Tsai H.-R., Chang S.-C.;

RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan."
 RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF138717; AAD33766.2; -.
 DR HSSP; P03485; 1AA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; FLU_M1; 1.
 DR Matrix protein; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1 1
 SQ SEQUENCE 239 AA; 26381 MW; B24B9F220299EC09 CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLE 8
 Db 216 LRDDLE 222

RESULT 9
 ID Q9WHY6 PRELIMINARY; PRT; 239 AA.
 AC Q9WHY6;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 GN M.
 OS Influenza A virus (A/Taiwan/98/21).
 OC ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
 OX NCBI_TAXID=94657;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/TAIWAN/98/21;
 RA Shih S.-R., Tsai H.-R., Chang S.-C.;
 RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan."
 RL EMBL; AF138716; AAD33765.2; -.
 DR HSSP; P03485; 1AA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; FLU_M1; 1.
 DR Matrix protein; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1 1
 SQ SEQUENCE 239 AA; 26298 MW; 6F8A4A4FBFC74BD CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLE 8
 Db 216 LRDDLE 222

RESULT 10
 ID Q9WHY5 PRELIMINARY; PRT; 239 AA.
 AC Q9WHY5;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 GN M.
 OS Influenza A virus (A/Taiwan/98/20).
 OC ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A and B group; Influenza A viruses.

OX NCBI_TAXID=94655;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/TAIWAN/97/3469;
 RA Shih S.-R., Tsai H.-R., Chang S.-C.;
 RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in Taiwan."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF138714; AAD33763.2; -.
 DR HSSP; P03455; 1AA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; FLU_M1; 1.
 DR Matrix protein; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1 1
 SQ SEQUENCE 239 AA; 26397 MW; 6E215E154BFFC64AC CRC64;

Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDLE 8
 Db 216 LRDDLE 222

RESULT 12
 ID Q9WHY3 PRELIMINARY; PRT; 239 AA.
 AC Q9WHY3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 GN M.
 OS Influenza A virus (A/Taiwan/98/20).
 OC ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A and B group; Influenza A viruses.

DE MATRIX PROTEIN M1 (FRAGMENT).
 GN Influenza A virus (A/Taiwan/97/3351).
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
 NCBI_TaxID=94654;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=A/TAIWAN/97/3351;
 RA Shih S.-R., Tsai H.-R., Chang S.-C.;
 RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 Taiwan.",
 RT Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AFL38713; AAD33762.2; -.
 DR HSSP; P03485; 1AA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR ProDom; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1 1
 SEQUENCE 239 AA; 26284 MW; 588AB82BB966975A CRC64;
 Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LRDDLE 8
 Db 216 LRDDLE 222
 RESULT 13
 Q9WHY1 PRELIMINARY; PRT; 239 AA.
 ID Q9WHY1
 AC Q9WHY1
 DT 01-NOV-1999 (TREMBrel. 12, Created)
 DT 01-MAR-2001 (TREMBrel. 12, Last annotation update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 GN Influenza A virus (A/Taiwan/96/2191).
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
 NCBI_TaxID=94652;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=A/TAIWAN/96/2191;
 RA Shih S.-R., Tsai H.-R., Chang S.-C.;
 RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 Taiwan.",
 RT Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AFL38711; AAD33760.2; -.
 DR HSSP; P03485; 1AA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR ProDom; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1 1
 SEQUENCE 239 AA; 26139 MW; 8151D148E9968759 CRC64;
 Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LRDDLE 8
 Db 216 LRDDLE 222
 RESULT 14
 Q9WHX9

DE MATRIX PROTEIN M1 (FRAGMENT).
 GN Influenza A virus (A/Taiwan/96/1600).
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
 NCBI_TaxID=94650;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=A/TAIWAN/96/1600;
 RA Shih S.-R., Tsai H.-R., Chang S.-C.;
 RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 Taiwan.",
 RT Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AFL38709; AAD33758.2; -.
 DR HSSP; P03485; 1AA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR ProDom; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1 1
 SEQUENCE 239 AA; 26407 MW; F8CAB96A8644455E CRC64;
 Query Match 81.0%; Score 34; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LRDDLE 8
 Db 216 LRDDLE 222
 RESULT 15
 Q9WHY2 PRELIMINARY; PRT; 250 AA.
 ID Q9WHY2
 AC Q9WHY2
 DT 01-NOV-1999 (TREMBrel. 12, Created)
 DT 01-MAR-2001 (TREMBrel. 12, Last annotation update)
 DE MATRIX PROTEIN M1 (FRAGMENT).
 GN Influenza A virus (A/Taiwan/96/3513).
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
 NCBI_TaxID=94653;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=A/TAIWAN/96/3513;
 RA Shih S.-R., Tsai H.-R., Chang S.-C.;
 RT "Sequence Analysis of M Gene of Influenza A Viruses Isolated in
 Taiwan.",
 RT Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AFL38712; AAD33761.1; -.
 DR HSSP; P03485; 1AA7.
 DR InterPro; IPR001561; -.
 DR Pfam; PF00598; Flu_M1; 1.
 DR ProDom; PD001061; -; 1.
 KW Matrix protein.
 FT NON_TER 1 1
 SEQUENCE 250 AA; 27671 MW; A47536C3B4C3FBC CRC64;
 Query Match 81.0%; Score 34; DB 14; Length 250;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Jul 10 13:30:21 2001

us-09-489-760-5.rspt

Page 6

Db 227 LRDDLE 233

Search completed: July 10, 2001, 08:36:07
Job time: 260 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:28:11 ; Search time 22.85 Seconds
(without alignments)
30.003 Million cell updates/sec

Title: US-09-489-760-2
Perfect score: 45

Sequence: 1 VLLDDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	84.4	1148	2 S51855	hypothetical prote
2	35	77.8	119	2 T00151	hypothetical prote
3	35	77.8	604	2 S36467	EL protein - human
4	35	77.8	605	2 S36469	EL protein - human
5	35	77.8	616	2 C68226	type I restriction
6	34	75.6	130	2 A81316	chemotaxis regulat
7	33	73.3	145	2 A41652	probable glyceroph
8	33	73.3	210	2 T44122	probable glyceroph
9	33	73.3	238	2 S78860	hypothetical prote
10	33	73.3	259	2 G82601	conserved hypothet
11	33	73.3	291	2 D83371	probable dehydroge
12	33	73.3	320	2 B73457	polypropeny synthas
13	33	73.3	322	2 C83075	ataprenyl-diphosp
14	33	73.3	343	2 A45351	DNA-directed DNA p
15	33	73.3	343	2 B85364	DNA polymerase III
16	33	73.3	378	2 T35403	probable polypropeny
17	33	73.3	397	2 S09013	hypothetical prote
18	33	73.3	398	2 H72660	probable N-Acylami
19	33	73.3	519	1 S69888	unspecific monooxy
20	33	73.3	519	2 S69889	PI protein - human
21	33	73.3	604	2 S36493	probable collagena
22	33	73.3	667	2 H85734	hypothetical prote
23	33	73.3	667	2 F64895	hypothetical prote
24	33	73.3	723	2 F85047	hypothetical prote
25	33	73.3	856	2 C85033	seca protein (imp
26	33	73.3	908	2 T50693	DNA repair and rec
27	33	73.3	973	2 S47449	MDM1 protein - Yea
28	33	73.3	1127	2 S56221	hypothetical prote
			1770	2	

RESULT	1	ALIGNMENTS			
	S51855				
		hypothetical protein YDR128w - yeast (Saccharomyces cerevisiae)			
		N; Alternative names: hypothetical protein YD9302_03			
		C; Species: Saccharomyces cerevisiae			
		C; Date: 05-May-1995 #sequence_revision 21-Jul-1995 #text_change 26-May-2000			
		C; Accession: S51855			
		R; Oliver, K.; Harris, D.			
		submitted to the EMBL Data Library, February 1995			
		A; Reference number: S51853			
		A; Accession: S51855			
		A; Molecule type: DNA			
		A; Residues: 1-1148 <OLI>			
		A; Cross-references: EMBL:248179; NID:9665657; PID:g665660; MIPS:YDR128w			
		C; Genetics:			
		A; Gen: MIPS:YDR128w			
		A; Map position: 4R			
		C; Superfamily: unassigned WD repeat proteins; WD repeat homology			

RESULT	2	ALIGNMENTS			
	T00151				
		hypothetical protein 18 - Staphylococcus aureus phage phi PVL			
		C; Species: Staphylococcus aureus phage phi PVL			
		C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000			
		C; Accession: T00151			
		R; Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kami, Y.			
		Biosci. Biotechnol. Biochem. 61, 1960-1962, 1997			
		A; Title: Panton-Valentine leukocidin genes in a phage-like particle isolated from ml			
		A; Residues: 1-119 <KAN>			
		A; Cross-references: EMBL:AB009866; NID:93341907; PID:BA316911; PID:g3341925			
		C; Superfamily: Staphylococcus aureus phage phi PVL hypothetical protein 18			

RESULT	2	ALIGNMENTS			
	QY				
		1 VLLDDLEA 9			
		:			
		Db 1001 LLLDDDEA 1009			

Db 72 HDDLEA 78
 |||:|||

RESULT 3

S36487 E1 protein - human papillomavirus type 19
 C;Species: human papillomavirus type 19
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Accession: S36487
 A;Molecule type: DNA
 A;Residues: 1-604
 A;Cross-references: EMBL:X74470; NID:9396940; PIDN:CAA52520.1; PID:9396943
 C;Superfamily: papillomavirus E1 Protein
 C;Keywords: early protein; nucleus

Query Match 77.8%; Score 35; DB 2; Length 604;
 Best Local Similarity 75.0%; Pred. No. 73;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDDLEA 9
 :|||||:
 Db 201 VHDDLES 208

RESULT 4

S36469 E1 protein - human papillomavirus type 14D
 C;Species: human papillomavirus type 14D
 C;Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
 R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Accession: S36469
 A;Molecule type: DNA
 A;Residues: 1-605
 A;Cross-references: EMBL:X74467; NID:9396918; PIDN:CAA52502.1; PID:9396919
 A;Experimental source: strain 14D
 C;Superfamily: papillomavirus E1 Protein
 C;Keywords: early protein; nucleus

Query Match 77.8%; Score 35; DB 2; Length 605;
 Best Local Similarity 75.0%; Pred. No. 73;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDDLEA 9
 :|||||:
 Db 202 VHDDLES 209

RESULT 5

C69226 type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicum
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
 C;Accession: C69226
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, J.; Aldredge, T.;
 Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function
 A;Reference number: A63000; MUID:98037514
 A;Accession: C69226
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
 A;Residues: 1-616 <NTH>
 A;Cross-references: GB:AE000868; GB:AE000666; PIDN:92622025; PID:92622025
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MTB942
 A;Start codon: ATG
 C;Superfamily: type I site-specific deoxyribonuclease chain nsdM

Query Match 77.8%; Score 35; DB 2; Length 616;
 Best Local Similarity 77.8%; Pred. No. 74;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLEA 9
 ||| 111:11
 Db 465 VLEDDLEA 473

RESULT 6

A81316 chemotaxis regulatory protein C1118c [Imported] - Campylobacter jejuni (strain NCTC
 C;Species: Campylobacter jejuni
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
 C;Accession: A81316
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanTieghem, A.; Whitehead, S.; Ba
 Nature 403, 665-668, 2000
 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
 A;Reference number: A81250; MUID:20150912
 A;Accession: A81316
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-130 <PAR>
 A;Cross-references: GB:AL139077; GB:AL111168; PIDN:96968444; PID:96968444
 A;Experimental source: serotype O2, strain NCTC 11168
 C;Genetics:
 A;Gene: chev; C1118c
 C;Superfamily: chemotaxis chev protein; response regulator homology

Query Match 75.6%; Score 34; DB 2; Length 130;
 Best Local Similarity 85.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDDLLEA 9
 |||:111
 Db 25 HDDVLEA 31

RESULT 7

A41652 probable glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - *Staphylococcus aureus*
 C;Species: *Staphylococcus aureus*
 C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 15-Oct-1999
 C;Accession: A41652
 R;Ryffel, C.; Bucher, R.; Kayser, F.H.; Berger-Baechi, B.
 J. Bacteriol. 173, 7416-7422, 1991
 A;Title: The *Staphylococcus aureus* mec determinant comprises an unusual cluster of di
 terase.
 A;Reference number: A41652; MUID:92041650
 A;Accession: A41652
 A;Molecule type: DNA
 A;Residues: 1-145 <RFX>
 A;Cross-references: GB:X52594; NID:948712; PIDN:CAA36830.1; PID:948713
 C;Keywords: phosphoric diester hydrolase

Query Match 73.3%; Score 33; DB 2; Length 145;
 Best Local Similarity 62.5%; Pred. No. 36;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLEA 8

Gendcore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:31:41; Search time 22.85 Seconds
(without alignments)
30.003 Million cell updates/sec

Title: US-09-489-760-5
Perfect score: 42

Sequence: 1 VLRDDEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0³

Maximum Match 100%
Listing first 45 summaries

Database: PIR_68:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35	83.3	616	2	C69226	type I restriction
2	34	81.0	282	2	S31258	probable membrane
3	34	81.0	343	2	A64443	glyceraldehyde-3-P
4	34	81.0	389	2	T20604	hypothetical prote
5	34	81.0	486	2	A82878	replicative DNA he
6	34	81.0	3519	2	S43048	polyketide synthas
7	33	78.6	300	2	D83714	surface adhesin A
8	33	78.6	324	2	T21672	quinone oxidoreduc
9	33	78.6	483	2	H85073	probable transposo
10	33	78.6	822	2	I38728	epidermal growth f
11	33	78.6	1041	2	E70760	two-component resp
12	32	76.2	237	2	D70032	hypothetical prote
13	32	76.2	264	2	T41578	hypothetical 37.8
14	32	76.2	335	2	A64988	probable oxidoredu
15	32	76.2	335	2	H85857	iron-sulfur cofact
16	32	76.2	372	2	D70753	hypothetical prote
17	32	76.2	389	2	T34766	hypothetical prote
18	32	76.2	452	2	T40769	leucyl aminopeptid
19	32	76.2	499	2	G86538	leucine aminopepti
20	32	76.2	499	2	G72083	probable phosphori
21	32	76.2	545	2	T00485	hypothetical prote
22	32	76.2	568	2	D83182	hypothetical prote
23	32	76.2	587	2	E71020	sulfite reductase
24	32	76.2	599	1	A34231	hypothetical prote
25	32	76.2	599	1	H65057	hypothetical prote
26	32	76.2	599	2	D85926	hypothetical prote
27	32	76.2	826	2	T46060	hypothetical prote
28	32	76.2	826	2	T46061	nitrate reductase
29	32	76.2	889	2	T02240	

30	32	76.2	1042	2	H75112	molybdenum cofacto
	31	73.8	112	2	S33180	nitrogen regulator
	32	73.8	244	2	D86725	hypothetical prote
	33	73.8	252	1	MFTVC	matrix protein M1
	34	73.8	252	1	B45539	matrix protein M1
	35	73.8	252	1	MFTVWS	matrix protein M1
	36	73.8	252	1	MFTVJK	matrix protein M1
	37	73.8	252	1	MFTVIF	matrix protein M1
	38	73.8	252	1	MFTVIM	matrix protein M1
	39	73.8	252	1	PNO083	matrix protein M1
	40	73.8	252	1	PNO086	matrix protein M1
	41	73.8	252	2	S04054	matrix protein M1
	42	73.8	252	2	S04052	matrix protein M1
	43	73.8	252	2	S04058	matrix protein M1
	44	73.8	252	2	S14616	matrix protein M1
	45	73.8	252	2		

ALIGNMENTS

RESULT 1	C69226	type I restriction modification enzyme, subunit M - Methanobacterium thermoautotroph
C; Species: Methanobacterium thermoautotrophicum		
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999		
C; Accession: C69226		
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T		
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, J.; Churchill, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.		
J. Bacteriol. 179, 715-715, 1997		
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu		
A; Reference number: A69000; MUID:98037514		
A; Accession: C69226		
A; Status: preliminary; nucleic acid sequence not shown; translation not shown		
A; Molecule type: DNA		
A; Residues: 1-616 <MTH>		
A; Cross-references: GB:AE000868; GB:AE000666; NID:92622025; PID:ABB85440,1; PID:9262		
A; Experimental source: strain Delta H		
C; GenBank:		
A; Gene: MTH942		
A; Start codon: GTG		
C; Superfamily: type I site-specific deoxyribonuclease chain hsdM		
RESULT 2	S31258	probable membrane protein FUN24 - yeast (Saccharomyces cerevisiae)
N; Alternative names: protein N2059; protein YN002c		
C; Species: Saccharomyces cerevisiae		
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001		
C; Accession: S31258; S5156; S48340; S63238		
R; Stettler, S.; Mariotte, S.; Riva, M.; Sentenac, A.; Thuriaux, P.		
J. Biol. Chem. 267, 21390-21395, 1992		
A; Title: An essential and specific subunit of RNA polymerase III (C) is encoded by g1		
A; Reference number: A45107; MUID:9316077		
A; Accession: S31258		
A; Status: nucleic acid sequence not shown; translation not shown		
A; Molecule type: DNA		
A; Residues: 1-282 <STP>		
A; Cross-references: EMBL:X63746; PID:94378; PID:CAA45279,1; PID:94380		
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, February 199		
R; Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.		
A; Submitted to the EMBL Data Library, January 1994		

A; Description: Twelve open reading frames revealed on the 23.6 kbp segment flanking the centromere. A; Reference number: S45126
 A; Accession: S45126
 A; Molecule type: DNA
 A; Cross-references: EMBL:X77395; NID:9496717; PIDN:CAA54571.1; PID:9496720
 A; Residues: 1-282 <VERS>
 A; Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
 Year 10: 1355-1361, 1994
 A; Title: Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere. A; Reference number: S48338; MUID:95208356
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-282 <VERS>
 A; Cross-references: EMBL:X77395; NID:9496717; PIDN:CAA54571.1; PID:9496720
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
 R; Aert, R.; Verhasselt, P.; Voet, M.; Volckaert, G.
 submitted to the Protein Sequence Database, April 1996
 A; Reference number: S62910
 A; Accession: S63328
 A; Molecule type: DNA
 A; Residues: 1-282 <AER>
 A; Cross-references: SGD:Z71617; NID:91302470; PIDN:CAA96278.1; PID:91302471; MIPS:YNRC
 A; Experimental source: strain S288C
 C; Genetics:
 A; Cross-references: SGD:S0005385; MIPS:YNR002C
 A; Map position: 14R
 A; Superfamily: Saccharomyces cerevisiae probable membrane protein FUN34
 C; Keywords: transmembrane protein
 C; Superfamily: Saccharomyces cerevisiae probable membrane protein FUN34
 F; 119-135/Domain: transmembrane #status predicted <TM1>
 F; 186-202/Domain: transmembrane #status predicted <TM2>
 F; 409-225/Domain: transmembrane #status predicted <TM3>
 F; 234-250/Domain: transmembrane #status predicted <TM4>

Query Match Score 81.0%; Best Local Similarity 87.5%; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 2 LRDDLEA 9 Db 62 LRDDLEFA 69

RESULT 3
 A64443
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Cross-references: GB:U67557; GB:L77117; PIDN:AB99147.1; PID:91591778; A; Map position: REV1086336-1085305
 C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase
 C; Keywords: oxidoreductase

Query Match Score 81.0%; Best Local Similarity 77.8%; Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Qy 2 LRDDLEA 9 Db 445 MRDDLEA 452

RESULT 4
 T20604
 A; Hypothetical protein Y51H1A.1 - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C; Accession: T20604; T27102
 R; Wallis, J.
 submitted to the EMBL Data Library, November 1996
 A; Reference number: Z19298
 A; Accession: T20604
 A; Status: preliminary; translated from GB/EMBL/IDB
 A; Molecule type: DNA
 A; Residues: 1-389 <NTL>
 A; Cross-references: EMBL:Z81495; PIDN:CRB04064.1; GSPDB:GN00020; CESP:Y51H1A.1
 A; Experimental source: clone F08G2
 R; Smye, R.
 submitted to the EMBL Data Library, October 1998
 A; Reference number: Z20309
 A; Accession: T21102
 A; Status: preliminary; translated from GB/EMBL/IDB
 A; Molecule type: DNA
 A; Residues: 1-389 <NTL>
 A; Cross-references: EMBL:AL032644; PIDN:CAA21673.1; GSPDB:GN00020; CESP:Y51H1A.1
 A; Experimental source: clone Y51H1A
 C; Genetics:
 A; Gene: CESP:Y51H1A.1
 A; Map position: 2
 A; Introns: 12/3; 38/3; 167/2; 276/1; 342/3

Query Match Score 81.0%; Best Local Similarity 87.5%; Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 2 LRDDLEA 9 Db 21 LRDELLEA 28

RESULT 5
 A82878
 A; Replicative DNA helicase U550 [imported] - *Ureaplasma urealyticum*
 C; Species: *Ureaplasma urealyticum*
 C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C; Accession: A82878
 R; Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A; Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a
 A; Reference number: A82870
 A; Accession: A82878
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-486 <GLA>
 A; Cross-references: GB:AE002153; GB:AE222894; NID:g6899544; PIDN:RAF30963.1; GSPDB:GN
 A; Experimental source: serovar 3; biovar 1
 C; Genetics:
 A; Gene: dnaB; UU550
 A; Genetic code: SGC3

Query Match Score 81.0%; Best Local Similarity 75.0%; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Qy 2 LRDDLEA 9 Db 445 MRDDLEA 452

A;Title: Evolutionary conservation of the EPS8 gene and its mapping to human chromosome 138728; MUID:94366758
 A;Accession: I38728
 A;Status: preliminary; translated from GB/EMBL/DBBJ
 A;Molecule type: mRNA
 A;Residues: 1-822 <RES>
 A;Cross-references: EMBL:U12535; NID:9530822; PID:9530823
 C;Genetics: EPS8
 A;Gene: EPS8
 C;Superfamily: SH3 homology

Query Match 78.6%; Score 33; DB 2; Length 822;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 E70760
 Probable IleS protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
 C;Accession: E70760
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Delvin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:9829987
 A;Accession: E70760
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-1041 <COL>
 A;Cross-references: GB:274020; GB:AL123456; NID:93261584; PID:CAA98326.1; PID:91403506
 C;Genetics:
 A;Gene: IleS
 C;Superfamily: isoleucine-tRNA ligase

Query Match 78.6%; Score 33; DB 2; Length 1041;
 Best Local Similarity 77.8%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VL RDDLEA 9
 Db 710 VL RDDLES 718

RESULT 12
 D70032
 two-component response regulator [YvcQ] homolog yvcP - Bacillus subtilis

C;Species: Bacillus subtilis
 C;Accession: D70032
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, A.; Bron, S.; Brouillet, S.; Calowell, B.; Capuano, V.; Carter, N.M.; Chacon, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
 A;Authors: Poulier, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fumia, S.; Galizzi, A.; Gallo, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullio, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarovic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, Y.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scandari, A.; Schleicher, S.; Schreeter, R.; Scoffone, F.; Sekiguchi, J.; Serowska, A.; Serov, Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, F.; Togoni, A.; Toscano, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yata, K.; Yasumoto, K.; Yoshida, N.

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome of the Gram-positive bacterium *Bacillus subtilis*
 A;Reference number: A69580; MUID:98044033
 A;Accession: D70032
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-237 <RUN>
 A;Cross-references: GB:299121; GB:AL009126; NID:92635827; PID:92635827
 A;Experimental source: strain 166
 C;Genetics:
 A;Gene: yvcP
 C;Superfamily: ompR protein; response regulator homology
 C;Keywords: phosphoprotein
 F;4-112/Domain: response regulator homology <RRH>
 F;52/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 76.2%; Score 32; DB 2; Length 237;
 Best Local Similarity 77.8%; Pred. No. 63;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 VL RDDLEA 9
 Db 176 VS RDLEEA 184

RESULT 13
 T41578
 hypothetical protein SPCC737.05 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
 C;Accession: T41578
 R;Murphy, L.; Harris, D.; Wood, V.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.
 A;Reference number: A70500; MUID:9829987
 A;Accession: E70760
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-264 <MR>
 A;Cross-references: EMBL:AL031546; NID:e1375214; PID:CAA44773.1; SPDB:GN00068; SPDB
 A;Experimental source: strain 972h()
 C;Genetics:
 A;Gene: SPCC737.05
 A;Map position: 3

Query Match 76.2%; Score 32; DB 2; Length 264;
 Best Local Similarity 55.6%; Pred. No. 71;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VL RDDLEA 9
 Db 26 IIR DELVEA 34

RESULT 14
 A64988
 hypothetical 37.8 kd protein in rplY-prol intergenic region - Escherichia coli (strain

C;Species: Escherichia coli
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
 C;Accession: A64988
 R;Blattner, R.B.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A;Rose, D.J.; Maur, B.; Shao, Y.; Science 277, 1453-1462, 1997
 A;Title: The complete genome of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617
 A;Accession: A64888
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-335 <BLAT>
 A;Cross-references: GB:AE000308; GB:U00096; NID:91788508; PID:AACT5247.1; PID:917885
 A;Experimental source: strain K-12, substrain MG1655
 C;Genetics:

RESULT	6	QY	1	VLRDDLE 8
S4 3048		Db	144	VLRDDLE 151
polyketide synthase type I - Streptomyces antibioticus				
C;Species: Streptomyces antibioticus				
C;Date: 13-Jan-1995 #sequence_revision 06-Dec-1996 #text_change 26-May-2000				
C;Accession: S41729				
C;Reference number: S43048				
A;Molecule type: DNA				
A;Residues: 1-519 <SWA>				
A;Cross-references: EMBL:09654; PIDN:AAA19695.1; PID:9153408				
R; Swan, D.G.; Rodriguez, A.M.; Vilches, C.; Mendez, C.; Salas, J.A.				
R; Salas, J.A.				
A;Title: Characterisation of a Streptomyces antibioticus gene encoding a type I polyketi				
A;Reference number: S41729; MUID:94150470				
A;Accession: S41729				
A;Status: nucleic acid sequence not shown				
A;Molecule type: DNA				
A;Residues: 1683-3238-3273-3303, 'K', 3305-3407, 'T', 3409-3462, 'Y', 3464-3516, 'E', 3518-3519				
A;Cross-references: EMBL:09654				
A;Start codon: GTG				
A;Superfamily: [acyl-carrier protein] S-malonyltransferase homology; 3'-oxoacyl-[acyl-car				
ogy; short-chain alcohol dehydrogenase homology				
C;Keywords: antibiotic biosynthesis; carrier protein				
F; 59-462/Domain: 3'-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>				
F; 570-851/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT1>				
F; 1202-181/Domain: short-chain alcohol dehydrogenase homology <SAD1>				
F; 1708-2111/Domain: acyl carrier protein homology <ACP1>				
F; 2882-2502/Domain: [acyl-carrier protein] S-malonyltransferase homology <AMT2>				
F; 3143-3214/Domain: short-chain alcohol dehydrogenase homology <SAD2>				
F; 3305-3500/Domain: oleoyl-[acyl-carrier-protein] hydrolase homology <ACPH>				
A;Cross-references: EMBL:09654				
QY	1	VLRDDLE 9		
Query Match	81.0%	Score 34; DB 2; length 3519;		
Best Local Similarity	87.5%	Pred. No. 4.7e+02;		
Matches	7;	Conservative 1; Mismatches 0;	Indels 0;	Gaps 0;
Db	770	LRDELLEA 777		
RESULT	7			
D83714				
D83714				
surface adhesin A precursor psaa [Imported] - Bacillus halodurans (strain C-125)				
C;Species: Bacillus halodurans				
C;Accession: D83714				
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai				
Nucleic Acids Res. 28, 4317-4331, 2000.				
A;Title: Complete genome sequence of the alkaliophilic bacterium Bacillus halodurans and				
A;Reference number: A83650; MUID:20263314				
A;Accession: D83714				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-300 <STO>				
A;Cross-references: GB:AP001508; GB:BA000004; PIDN:g10172890; PIDN:BA04235.1; GSPDB:GN00				
A;Experimental source: strain C-125				
C;Genetics:				
C;Gene: Psaa				
C;Superfamily: adhesin B				
RESULT	10			
I38728				
epidermal growth factor receptor kinase substrate - human				
C;Species: Homo sapiens (man)				
C;Accession: I38728				
R; Mong, W.T.; Carliomagno, F.; Druck, T.; Barletta, C.; Croce, C.M.; Huebner, K.				
Oncogene 9, 3057-3061, 1994				
QY	1	VLRDDLE 7		
Query Match	78.6%	Score 33; DB 2; length 300;		
Best Local Similarity	75.0%	Pred. No. 52;		
Matches	6;	Conservative 2; Mismatches 0;	Indels 0;	Gaps 0;
Db	145	VLRDDLE 151		

DT	01-NOV-1996	(TREMBLrel. 01, Created)	Q9VA13	PRELIMINARY;	PRT;	774 AA.
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	ID	Q9VA13;		
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)	AC	Q9VA13;		
DE	C-TERMINAL SEQUENCE OF ORF C PRODUCT SHOWS HOMOLOGY TO SEVERAL	DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DE	TERMINAL ORFS.	DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
OS	Leishmania donovani.	DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		
OC	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatida; Leishmania.	DE	CG11318	PROTEIN.		
OX	NCBI_TAXID=5661;	GN	CG11318.			
RN	[1]	OS	Drosophila melanogaster (Fruit fly).			
RP	SEQUENCE FROM N.A.	OC	Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
STRAIN	MHOM/BL/67/IMMAP263;	OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
RX	MEDLINE=95047445; PubMed=7958944;	OC	Ephydioidea; Drosophilidae; Drosophila.			
RX	PFAM; PF00849; Pseudoo_synth_2; 1.	OX	NCBI_TAXID=7227;			
RT	"A frequently amplified region in Leishmania contains a gene conserved	RN	111			
RT	in prokaryotes and eukaryotes.";	RP	SEQUENCE FROM N.A.			
DR	EMBL; U02459; AAA64631; 1; -.	RC	MEDLINE=20196006; PubMed=10731132;			
DR	InterPro; IPR000613; -.	RA	Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
DR	IntPfam; IPR002990; -.	RA	Amatiades P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
DR	ProDom; PDD001819; ; 1.	RA	George R.A., Lewis S.E., Richards S.J., Ashburner M., Henderson S.N.,			
DR	ProSITE; PS01129; PSI_RLU; 1.	RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
SQ	SEQUENCE 741 AA; 80050 MW;	RA	Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Chang M., Pfeiffer B.D.,			
QY	Query Match 75 6%; Score 34; DB 5%; Length 741;	RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,			
QY	Best Local Similarity 62.5%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;	RA	Abrial J.F., Agyapanyi A., An H.-J., Andrews P.-Fannkuch C., Baldwin D.,			
DB	2 LHDDLEA 9	RA	Ballew R.M., Basu A., Boxendale J., Bayraktaroglu L., Beasley E.M.,			
DB	628 LHDDIDA 635	RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RESULT	9	RA	Borkova D., Borkstein M.R., Bouch J., Brockstein P., Brodtier P.,			
Q9NDK7	SEQUENCE FROM N.A.	RA	Bortz K.C., Busam D.A., Butler H., Cadine B., Chandra I.,			
ID	Q9NDK7	RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
AC	Q9NDK7;	RA	De Pablos B., Delcher A., Deng Z., Dietz S.M.,			
DT	01-OCT-2000	(TREMBLrel. 15, Created)	RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)	RA	Dubrin K.J., Evangelista C., Ferraz C., Ferreira S., Glasser K.,		
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)	RA	Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glässer K.,		
DE	511.8.	RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
DE	511.8.	RA	Harris N.L., Harvey D., Heimland T.J., Hernández J.R., Houck J.,			
OS	Leishmania major.	RA	Houston D., Houston K.A., Howland T.J., Wei M.-H., Ibargam C.,			
OC	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatida; Leishmania.	RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
OX	NCBI_TAXID=5664;	RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RN	[1]	RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RP	SEQUENCE FROM N.A.	RA	Merkulov G., Milshina N.V., Mobarrey C., Morris J., Mosheri A.,			
STRAIN	MHOM/BL/67/IMMAP263;	RA	Mount S.M., Moy M., Murphy B., Nixon K.A., Nelson D.L.,			
RX	MEDLINE=95047445; PubMed=7958944;	RA	Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pollard J., Puri V., Reese M.G.,			
RX	PFAM; PF00849; Pseudoo_synth_2; 1.	RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RT	"The genome sequence of Drosophila melanogaster.";	RA	Shieh B.C., Sider-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RT	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,	RA	Swanson R., Tector C., Turner R., Venter E., Wang A.-H., Wang X.,			
RA	Cawthray J., Marsolini F., Sunkin S., Stuart K.D., Cunningham M.,	RA	Wang Z.-Y., Wasserman D.A., Weissenbach J.,			
RA	Beverley S.,	RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	RL	RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,			
DR	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	RA	Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,			
DR	EMBL; AC005801; AAF77202.1; -.	RA	Science 28:2185-2196 (2000).			
DR	InterPro; IPR000613; -.	RA	DR	AE005776; AAF57115.1; -.		
DR	InterPro; IPR002990; -.	RA	DR	FLYBase; Fgn0039816; CG11318.		
DR	PROSITE; PS00190; CRYPTOCHROME_C; UNKNOWN_1.	RA	DR	InterPro; IPR000203; -.		
DR	PROSITE; PS01129; PSI_RLU; 1.	RA	DR	PFAM; PF00002; 7tm_2; 1.		
SQ	SEQUENCE 741 AA; 79890 MW;	RA	DR	PRINTS; PRO0249; GPCSECRETIN.		
QY	2 LHDDLEA 9	RA	DR	SMART; SM0303; GPS; 1.		
Db	628 LHDDIDA 635	RA	DR	SEQUENCE 74 AA; 87359 MW;		
RESULT	10	RA	Query Match 75 6%; Score 34; DB 5%; Length 741;	75.6%	Score 34;	DB 5;
QY	Best Local Similarity 62.5%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;	RA	Best Local Similarity 85.7%; Pred. No. 3.2e+02;	85.7%	Length 774;	
Db	2 LHDDLEA 9	RA	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	1		
Db	628 LHDDIDA 635	RA	Qy 2 LHDDLEA 9	111111		
Db	121 LHDDVLE 127	RA	Qy 121 LHDDVLE 127	111111		

OX NCBI_TaxID=6239;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=415018; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A., Craxton M., Dear S., Burton J., Connell M., Copsey T., Cooper J., Fulton L., Gardner A., Green P., Hawkins T., Dublin R., Favello A., Fulton L., Jones M., Keirshaw J., Kierster J., Hillier L., Jier M., Johnston L., Lightning J., Lloyd C., McMurry A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen R., Saldanha N., Smith A., Sonnhammer E., Staden R., Stalston J., Thierry-Mieg J., Thomas K., Vaughn M., Waterston R., Watson A., Weinstock L., Wilkison-sprott J., Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN=BRISTOL N2;
 RA Geisel C., Bradshaw H.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR InterPro:IPR00004; -.
 DR SMART: SM00118; SAPB: 1.
 SQ SEQUENCE 174 AA; 19210 MW; A6303CF6383BBD9 CRC64;
 Query Match 73.3%; Score 33; DB 5; Length 174;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLHDLLPA 9
 11 111:1
 Db 129 VLKDDLLDA 137

RESULT 14
 Q9RPT9 PRELIMINARY; PRT; 175 AA.
 AC Q9RPT9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 20.3 KDa PROTEIN.
 OS Streptomyces albus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Streptomyctaceae; Streptomyces.
 OX NCBI_TaxID=1888;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=ATCC21838;
 RA Kwon H.-J., Lee S.-Y., Hong S.-K., Park U.-M., Suh J.-W.;
 RT "Heterologous Expression of Streptomyces albus Genes Linked to an Integrating Element and Activation of Antibiotic Production.";
 RL J. Microbiol. Biotechnol. 9:488-497(1999).
 DR AF145724; AAD46513; -.
 DR InterPro:IPR000182;
 DR PRO058; Acetyltransfer; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 175 AA; 20300 MW; 22A46EA40732DD0A CRC64;

Query Match 73.3%; Score 33; DB 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HDLLE 8
 Db 33 HDLLE 18

A;Gene: yejk

Query Match Score 32; DB 2; Length 335;
 Best Local Similarity 87.5%; Pred. No. 92;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRRDLLE 8
 ||||| |||
 Db 24 VLRSLSLE 31

RESULT 15

H85857 hypothetical protein yejk (imported) - Escherichia coli (strain O157:H7)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C;Accession: H85857

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, R.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potanousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; PMID:21074935; PMID:11206551

A;Accession: H85857

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-335 <STO>

A;Cross references: GB:AE005174; NID:gi:2516518; PIDN:AGS57324.1; GSPPDB:GN00145; UNIGP:234

A;Experimental source: strain O157:H7, subspecies EDL933

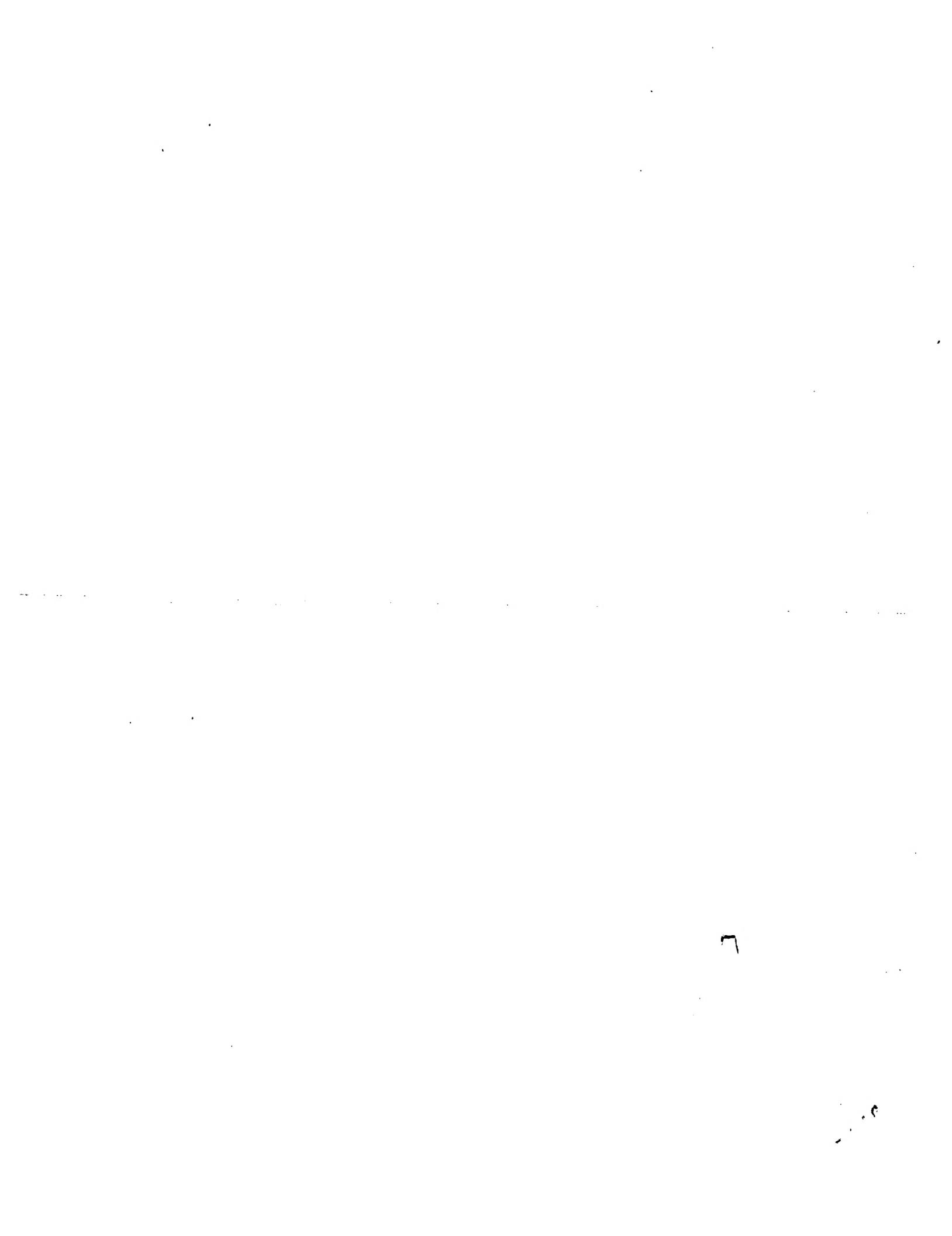
C;Genetics:

A;Gene: yejk

Query Match Score 32; DB 2; Length 335;
 Best Local Similarity 87.5%; Pred. No. 92;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRRDLLE 8
 ||||| |||
 Db 24 VLRSLSLE 31

Search completed: July 10, 2001, 08:31:41
 Job time: 210 sec



Db 48 IHHDDYLE 55
 A;Accession: G82601
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-259 <SIM>
 A;Cross-references: GB:AE004024; GB:AE003849; PIDN:AAF84889.1; GSPDB:GN
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Aruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, A.P.; Ferreira, A.J.S.
 R;Ito, T.; Katayama, Y.; Hiranatsu, K.
 C;Accession: T44122
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 11-May-2000
 C;Species: *Staphylococcus aureus*
 C;Antimicrob. Agents Chemother. 43, 1449-1458, 1999
 A;Title: Cloning and nucleotide sequence determination of the entire *meC* DNA of *pre-meth*
 A;Reference number: 222733; MUID:98278010
 A;Accession: T44122
 A;Species: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-210 <ITR>
 A;Cross-references: EMBL:D86934; PIDN:BAA82224.1
 A;Experimental source: strain N315
 C;Keywords: phosphoric diester hydrolase
 A;GenBank accession number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XF2090

RESULT 8
 Query Match 73.3%; Score 33; DB 2; Length 210;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy :||| | |
 Db 48 IHHDDYLE 55

RESULT 9
 S76860 hypothetical protein s11549 - *Synechocystis* sp. (strain PCC 6803)
 C;Species: *Synechocystis* sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C;Accession: S76860
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
 s.
 A;Reference number: S74322; MUID:97061201
 A;Accession: S76860
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-238 <KAN>
 A;Cross-references: EMBL:D90917; GB:AB001339; PIDN:91653836; PIDN:BAA18772.1; PID:d101950
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

RESULT 10
 GB2601 conserved hypothetical protein XF2090 (imported) - *Xylella fastidiosa* (strain 9a5c)
 C;Species: *Xylella fastidiosa*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: G82601
 R;Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A;Reference number: AB2515; MUID:206517
 A;Note: for a complete list of authors see reference number A59328 below

RESULT 11
 D83371 probable dehydrogenase PA2199 (imported) - *Pseudomonas aeruginosa* (strain PA01)
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: D83371
 R;Stover, C.K.; Pham, Y.Q.; Erwin, R.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
 Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.;
 Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa
 A;Reference number: A82950; MUID:20437337
 A;Accession: D83371
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-291 <STOP>
 A;Cross-references: GB:AE004646; GB:AE004091; PIDN:99948213; PIDN:AAG05587.1; GSPDB:G1
 C;Genetics:
 A;Gene: PA2199

RESULT 12
 B73457 polyphenyl synthase - *Deinococcus radiodurans* (strain R1)
 C;Species: *Deinococcus radiodurans*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C;Accession: B73457
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
 M.; Shan, M.; Yamashita, J.; Lau, P.; McDonald, L.; Utterback, T.; Zalewski, C.
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999
 A; Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A; Reference number: A75250; MUID:20036836
 A; Accession: B75457
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-320 <WHI>
 A; Cross-references: GB:AE001946; GB:AE000513; NID:96458655; PIDN:AAF10509.1; PID:96458655
 A; Experimental source: strain R1
 C; Genetics:
 A; Gene: DR0932
 A; Map position: 1
 C; Superfamily: prenyl transferase A

Query Match 73.3%; Score 33; DB 2; Length 320;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHLDDLE 8
 Db 79 LLHDDLD 86

RESULT 1.3
 C83075 octaprenyl-diphosphate synthase PA4569 [Imported] - *Pseudomonas aeruginosa* (strain PA01)
 C; Species: *Pseudomonas aeruginosa* aeruginosa (strain PA01)
 C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
 C; Accession: C83075
 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brachman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A; Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A; Reference number: A82950; MUID:20437337
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-322 <SMQ>
 A; Cross-references: GB:AE004870; GB:AE004091; NID:99950807; PIDN:AGG07957.1; GSPDB:GN001
 A; Experimental source: strain PA01
 C; Genetics:
 A; Gene: ispb; PA4569
 C; Superfamily: prenyl transferase A

Query Match 73.3%; Score 33; DB 2; Length 320;
 Best Local Similarity 55.6%; Pred. No. 87;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHLDDLE 8
 Db 79 LLHDDLD 86

RESULT 1.3
 C83075 octaprenyl-diphosphate synthase PA4569 [Imported] - *Pseudomonas aeruginosa* (strain PA01)
 C; Species: *Pseudomonas aeruginosa* aeruginosa (strain PA01)
 C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
 C; Accession: C83075
 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brachman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A; Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A; Reference number: A82950; MUID:20437337
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-322 <SMQ>
 A; Cross-references: GB:AE004870; GB:AE004091; NID:99950807; PIDN:AGG07957.1; GSPDB:GN001
 A; Experimental source: strain PA01
 C; Genetics:
 A; Gene: ispb; PA4569
 C; Superfamily: prenyl transferase A

Query Match 73.3%; Score 33; DB 2; Length 322;
 Best Local Similarity 55.6%; Pred. No. 87;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHLDDLEA 9
 Db 81 LLHDDVYDA 89

RESULT 1.4
 A45251 DNA-directed DNA polymerase (EC 2.7.7.7) III delta chain - *Escherichia coli*
 C; Species: *Escherichia coli*
 C; Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C; Accession: A45251; A46738; F64798
 R; Carter, J.R.; Franden, M.A.; Aebersold, R.; McHenry, C.S.
 A; Title: Molecular cloning, sequencing, and overexpression of the structural gene encod
 A; Reference number: A45251; MUID:93015786
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: nucleic acid
 A; Residues: 1-343 <CAR>
 A; Cross-references: GB:MM94267; NID:9145784; PIDN:AB59047.1; PID:g145785
 A; Note: sequence extracted from NCBI backbone (NCBIP:117007)
 R; Dong, Z.; Onrust, R.; Skangalis, M.; O'Donnell, M.

J. Biol. Chem. 268, 11758-11765, 1993
 A; Title: DNA polymerase III accessory proteins. I. holB encoding delta and
 A; Reference number: A46738; MUID:93280136
 A; Accession: A46738
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-343 <DON>
 A; Cross-references: GB:LO4576; NID:9145728; PIDN:AAA3675.1; PID:g145729
 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1433-1462, 1997
 A; Title: The complete genome sequence of *Escherichia coli* K-12.
 A; Reference number: A64720; MUID:97426617
 A; Accession: F64798
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-343 <BLAT>
 A; Cross-references: GB:AB00168; GB:U00096; NID:91786849; PIDN:AA73741.1; PID:g17868
 A; Experimental source: strain K-12, substrain MG1655
 C; Genetics:
 A; Gene: holA
 C; Complex: DNA polymerase III is a multichain complex; alpha, epsilon, theta, tau, gamma
 C; Function: <GEN>
 A; Description: DNA synthesis; synthesizes both, the lagging and the leading strands
 A; Pathway: DNA biosynthesis
 A; Note: core enzyme (catalytic core) contains chains alpha, epsilon and theta; alpha required for assembly; tau allows dimerization of the core complex and processivity to; the holoenzyme is completed by addition of beta chain which clamps the enzyme to
 C; Function: <DEB>
 A; Description: delta chain seems to interact with the gamma chain
 A; Note: gamma/delta complex is composed of chains gamma, delta, epsilon, tau, psi and chi
 C; Keywords: DNA biosynthesis; DNA replication; nucleotidyltransferase

Query Match 73.3%; Score 33; DB 2; Length 343;
 Best Local Similarity 85.7%; Pred. No. 93;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHLDDLL 7
 Db 103 LLHDDLL 109

RESULT 15
 B85564 DNA polymerase III, delta subunit [Imported] - *Escherichia coli* (strain O157:H7)
 C; Species: *Escherichia coli*
 C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 C; Accession: B85564
 R; Perna, N.T.; Plunkett III, G.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhiller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apode
 Nature 409, 529-533, 2001
 A; Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A; Reference number: A85480; MUID:11206551
 A; Accession: B85564
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-343 <SMO>
 A; Cross-references: GB:AE005174; NID:912513544; PIDN:AAG54974.1; GSPDB:GN00145; UWGP
 A; Experimental source: strain O157:H7, substrain EDL933
 C; Genetics:
 A; Gene: holA

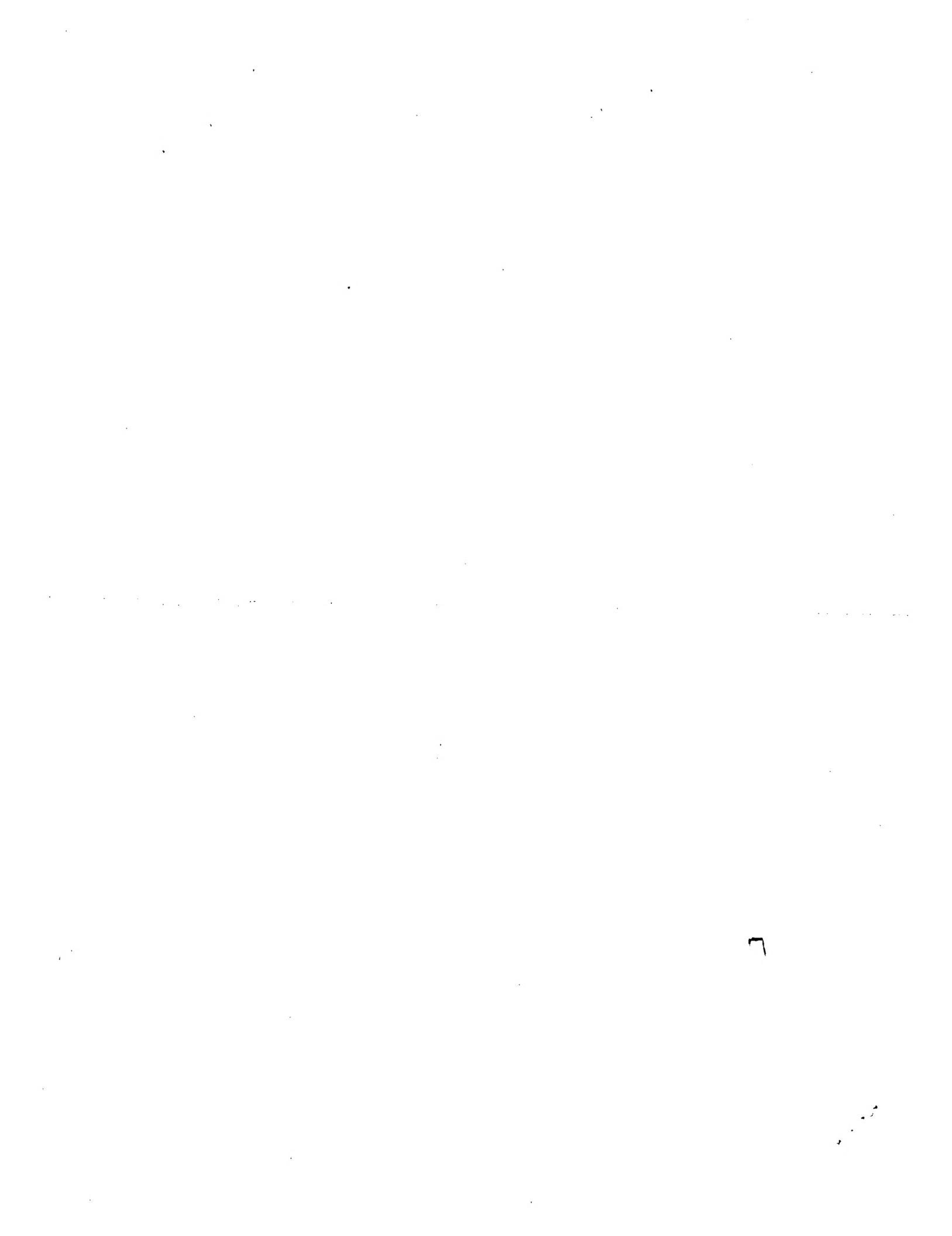
Query Match 73.3%; Score 33; DB 2; Length 343;
 Best Local Similarity 85.7%; Pred. No. 93;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHLDDLL 7
 Db 103 LLHDDLL 109

Tue Jul 10 13:30:14 2001

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Page 5

Search completed: July 10, 2001, 08:31:41
Job time: 210 sec



STRAIN=ATCC 55026 / 81-176;
 RX PDBLINE=97231343; PubMed=9076738;

RA Yao R., Burr D.H., Guerry P.;
 "CheY-mediated modulation of *Campylobacter jejuni* virulence.";

RT Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 Gregor J., Davis N.W., Kirpatrick H.A., Goeden M.A., Rose D.J.,
 Mau B., Shao Y.;

RL "The complete genome sequence of *Escherichia coli* K-12.";
 CC Science 277:1453-1474(1997).

CC THE CLOCKWISE (CW) ROTATION (BY SIMILARITY).
 CC SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE RESPONSE REGULATORY FAMILY.

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CC EMBL: U75208; AAB17571.1; -.
 DR EMBL; AL1648; CAA72347.1; -.
 DR EMBL; AL13907; CAB7337.1; -.
 DR EMBL; U62038; AAC44858.1; -.
 DR EMBL; P06143; ICEY.
 DR InterPro; IPR01789; -.
 DR Pfam; PF00072; response_reg; 1.
 KW Chemosensitivity; Sensory transduction; Phosphorylation; Flagellar rotation.
 FT DOMAIN 1 119 RECEIVER DOMAIN (POTENTIAL).
 FT MOD_RES 53 53 PHOSPHORYLATION (BY SIMILARITY).
 SEQUENCE 130 AA; 14437 MW; 41634D8ADE6C3081 CRC64;

Query Match 75.6% Score 34; DB 1; Length 130;
 Best Local Similarity 85.7%; Pred. No. 6.3;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDDLLEA 9
 Db 25 HDDLLEA 31

RESULT 5
 ID HOIA_ECOLI
 AC P28630;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DE DNA POLYMERASE III, DELTA SUBUNIT (EC 2.7.7.)
 GN HOIA.
 OS *Escherichia coli*,
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 RN [1] TAXID=562;
 RP SEQUENCE FROM N.A.
 STRAIN=K12;
 RX PDBLINE=93200136; PubMed=8505303;
 RA Dong Z., Onrust R., Skangalis M., O'Donnell M.;
 "DNA polymerase III accessory proteins. I. *holA* and *holB* encoding
 delta and delta'";
 RL J. Biol. Chem. 268:11758-11765(1993).

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=MAF102;
 RX PDBLINE=93015766; PubMed=1400251;
 RA Carter J.R., Fraiden M.A., Aebersold R.H., McHenry C.S.;
 "Molecular cloning, sequencing, and overexpression of the structural
 gene encoding the delta subunit of *Escherichia coli* DNA polymerase
 III holoenzyme.";
 RL J. Bacteriol. 174:7013-7025(1992).

RN [3] SEQUENCE FROM N.A.
 RP

SEQUENCE FROM N.A.
 RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
 Komp C., Kurdi O., Lew H., Lin D.,
 Federer P., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 Namath A., Oefner P., Robert D., Schramm S., Davis R.W.,
 Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

[5] SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX PDBLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 Ikemoto K., Inada T., Itoh T., Kajihara M., Karai K., Kashimoto K.,
 Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 Mori H., Motomura K., Nakamura Y., Nishio Y., Saito N.,
 Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 Yano M., Horuchi T.;
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
 corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 RN [6] PRELIMINARY SEQUENCE OF 1-49 FROM N.A.
 RP PRELIMINARY SEQUENCE OF 1-49 FROM N.A.
 RC STRAIN=K12;
 RX PDBLINE=88058785; PubMed=3316191;
 RA Takase I., Ishino F., Wachi M., Kamata H., Doi M., Asoh S.,
 Matsuzawa H., Ohta T., Matsushashi M.;
 RT "Genes encoding two lipoproteins in the leuS-dacA region of the
Escherichia coli chromosome.";
 RL J. Bacteriol. 169:5692-5699(1987).
 RN [7] CHARACTERIZATION.
 RX PDBLINE=3280137; PubMed=8505304;
 RA Onrust R., O'Donnell M.;
 RT "DNA polymerase III accessory proteins. II. Characterization of delta
 and delta'";
 RL J. Biol. Chem. 268:11766-11772(1993).
 RN [8] REVIEW.
 RX PDBLINE=9246502; PubMed=1575709;
 RA O'Donnell M.;
 RT "Accessory protein function in the DNA polymerase III holoenzyme from
E. coli";
 RL Bioessays 14:105-111(1992).
 CC -!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
 CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
 CC THIS DNA POLYMERASE ALSO EXHIBITS 3'-TO 5' EXONUCLEASE ACTIVITY.
 CC THE DELTA SUBUNIT SEEMS TO INTERACT WITH THE GAMMA SUBUNIT TO
 CC TRANSFER THE BETA SUBUNIT ON THE DNA.
 CC -!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
 CC N PYROPHOSPHATE + DNA(N).
 CC -!- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
 CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
 CC DIMERIZATION TO FORM THE POLII COMPLEX. POLII ASSOCIATES WITH
 CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
 CC AND CHI) AND WITH THE BETA CHAIN. THE FINAL COMPOSITION OF THE
 CC COMPLEX IS: (ALPHA, EPSILON, THETA)[2]-TAU[2] (GAMMA, DELTA, DELTA',
 CC PSI, CHI)[2]-BEI[4].
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 CC ---

DS	Candida apicola (yeast).
DC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
DC	Saccharomycetales; mitosporic Saccharomycetales; Candida.
DX	NCBI_TaxID=29830;
RN	[1]
SEQUENCE FROM	N.A.
STRAIN	IMET 437/7;
RP	96-36759/7; PubMed=8771711;
RC	Lottermoser K.; Schunck W.H.; Asperger O.;
RRX	"Cytocromes P450 of the sophorase lipid-producing yeast Candida apicola: heterogeneity and polymerase chain reaction-mediated cloning of two genes." Yeast 12:565-571(1996).
RT	1 - SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
RL	
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```

C EMBL; X76225; CAA53811.1; -
C DR; IPR001128; -
C DR; IPR002402; -
C DR; IPR002974; -
C PRIMT; PF0067; p50; 1.
C PRINTS; PR00464; EP4501I.
C PRINTS; PRO1239; EP4501ICP52.
C DR; PS00086; CYTOCHROME_P450; 1.
C PROSITE; PS00086; CYTOCHROME_P450; 1.
C KW; Electron transport; Oxidoreductase; Heme;
C KW; Transmembrane;
C TRANSMM; 10 30 POTENTIAL.
C FPT; TRANSMEM 44 64 POTENTIAL.
C FPT; BINDING 479 479 Heme (by SIMILARITY).
C SEQ; 519 AA; 58656 MW; 4185235A07EA4370 CRC64;

Query Match 73.38; Score 33; DB 1; Length 519;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 0; Indels 0;
Gaps 0;

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RESULT		9	
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AC	Q12573;		519 AA.
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DTT	15-DEC-1998	(Rel. 37, Last annotation update)	
CYTOCHROME	P450_52E2	(EC 1.14.14.1) (CYPLIE2).	
GN	CYP52E2.		
OS	Candida apicola (Yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Candida.		
OC	Saccharomycotina; mitosporic Saccharomycetales; Candida.		
NCBI_TAXID	29830;		
DX			11

SEQUENCE FROM N.A.
STRAIN=IMET 43747;
MEDLINE=96367597; PubMed=8771711;
LITERATUREREFERENCE K.; Schunck W.H.; Asperger O.;
"Cytochromes P450 of the sophorase lipid-producing yeast *Candida*
apicola: heterogeneity and polymerase chain reaction mediated cloning
of two genes.";
Yeast 12:565-575(1996).
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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EMBL; X8640; CA64940.1; -;	DR	InterPro; IPR001128; -;
InterPro; IPR002402; -;	DR	InterPro; IPR002974; -;
InterPro; IPR002974; -;	DR	pFam; PF00067; P450; 1;
pFam; PF00067; P450; 1;	DR	PRINTS; PRO0464; EP05011;
PRINTS; PRO0464; EP05011;	DR	PRINTS; PRO1239; EPAS0110YP52;
PRINTS; PRO1239; EPAS0110YP52;	DR	PROSITE; PS00086; CYTOCHROME_P450; 1;
PROSITE; PS00086; CYTOCHROME_P450; 1;	KW	Electron transport; Oxidoreductase; Monoxygenase; Heme;
Electron transport; Oxidoreductase; Monoxygenase; Heme;	KW	Transmembrane.
Transmembrane.	FT	TRANSMEM 10 30 POTENTIAL.
TRANSMEM 10 30 POTENTIAL.	FT	TRANSMEM 44 64 POTENTIAL.
TRANSMEM 44 64 POTENTIAL.	FT	BINDING 461 461 HME (BY SIMILARITY).
BINDING 461 461 HME (BY SIMILARITY).	SQ	SEQUENCE 519 AA; 58631 MW; F0B164E222D169C86 CRC64;
SEQUENCE 519 AA; 58631 MW; F0B164E222D169C86 CRC64;	RESULT	10
VE1_HPV25	VE1_HPV25	STANDARD; PRT; 604 AA.
ID	VE1_HPV25	STANDARD; PRT; 604 AA.
Q02049;		
AC		
DT 01-JUL-1993 (Rel. 26, Created)		
DT 01-JUL-1993 (Rel. 29, Last sequence update)		
DT 15-JUL-1998 (Rel. 36, Last annotation update)		
DE REPLICATION PROTEIN E1.		
E1.		
OS Human papillomavirus type 25.		
OS Viruses; ssDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.		
[1]		
RN SEQUENCE FROM N.A.		
RP MEDLINE=94265501; PubMed=8205838;		
RX		
RA Delius H., Hofmann B.;		
RA RT primer-directed sequencing of human papillomavirus types. ".		
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).		
RN [2]		
RN SEQUENCE OF 331-382 FROM N.A.		
RX MEDLINE=92407963; PubMed=1326639;		
RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Birgit H., Delius H.,		
RA RT Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and		
RT variants: a showcase for the molecular evolution of DNA viruses. ".		
RL J. Virol. 66:5714-5725(1992).		
RL - FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF		
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2		
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH		
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.		
CC - SUBCELLULAR LOCATION: NUCLEAR.		
CC		
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CC		
CC EMBL; X74471; CAA52526.1; -;		
DR EMBL; M96321; AAA47010.1; -;		

DR PIR: S36493; S36493.
 DR INTRPRO; IPRO01177; -.
 DR Pfam: PF00519; El; 1.
 DR Pfam: PF00524; El_N; 1.
 DR Early protein; DNA replication; Helicase; ATP-binding; DNA-binding; Nuclear protein.
 KW NUCLEAR PROTEIN.
 FT NP_BIND 432 ATP (POTENTIAL)
 SQ SEQUENCE 604 AA; 68925 MW; 0A98EB84E93B19B9 CRC64;
 Query Match 73.3%; Score 33; DB 1; Length 604;
 Best Local Similarity 62.5%; Pred. No. 56;
 Matches 5; Conservative 3; Mismatches 0; Gaps 0;
 Indels 0;
 QY 2 LHDDLEA 9
 Db 201 VHDDLIES 208
 RESULT 1.1
 YDCP_ECOLI STANDARD; PRT; 653 AA.
 ID YDCP_ECOLI
 AC P76104; P76867; P76865;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PUTATIVE PROTEASE YDCP PRECURSOR (EC 3.4.-.-).
 GN YDCP.
 OC Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=K12 / MG1655;
 RC MEDLINE=97426617; PubMed=9278503;
 RX Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rose C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.,
 RA "The complete genome sequence of Escherichia coli K-12.";
 RA Science 277:1453-1474 (1997).
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Baba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sampei G., Seki Y., Sivansundaram S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horuchi T.,
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map."
 RL DNA Res. 363:377 (1996).
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 32.
 CC
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 CC
 DR EMBL; AE00240; AAC74517.1; ALT_INIT.
 DR EMBL; D90782; BAA15063.1; -.
 DR EMBL; D90783; BAA15068.1; -.
 DR EMBL; D90784; BAA15074.1; -.
 DR Ecocline; EC1759; ydcP.
 DR InterPro; IPR001539; -.
 DR Pfam; PF01136; Peptidase_U32; 1.
 DR

DR PROSITE; PS01276; PEPTIDASE_U32; 1.
 KW HYPOTHETICAL PROTEIN; HYDROLASE; PROTEASE; SIGNAL.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 653 PUTATIVE PROTEASE YDCP.
 SQ SEQUENCE 653 AA; 72701 MW; 5875B4E9C24FC82 CRC64;
 Query Match 73.3%; Score 33; DB 1; Length 653;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 1; Indels 0;
 Gaps 0;
 QY 1 VLHDDLE 8
 Db 72 VLHDDLE 79
 RESULT 1.2
 RI15_YEAST STANDARD; PRT; 1770 AA.
 ID RI15_YEAST
 AC P43565;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE SERINE/THEONINE-PROTEIN KINASE RIM15 (EC 2.7.1.-).
 GN RIM15 OR TAK1 OR YEL033C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
 OC Saccharomycetales; Saccharomyctaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=S288C / AB972; PubMed=7670463;
 RX MEDLINE=9540029; PubMed=7670463;
 RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
 RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
 RA Yamazaki M., Tashiro H., Eki T.;
 RT "Analysis of the nucleotide sequence of chromosome VI from
 RT Saccharomyces cerevisiae.";
 RL Nat. Genet. 10:261-268 (1995).
 RN [2] SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RX MEDLINE=97265402; PubMed=9111339;
 RA Vidan S., Mitchell A.P.;
 RA "Stimulation of yeast meiotic gene expression by the
 RT glucose-repressible protein kinase Rim15p.";
 RL Mol. Cell. Biol. 17:2688-2697 (1997).
 RN [3] SEQUENCE FROM N.A.
 RP
 RA Reinders A., Buerkert N., Boller T., Wiemken A., de Virgilio C.;
 RA "Saccharomyces cerevisiae cAMP dependent protein kinase controls entry
 RT into stationary phase through the Rim15p protein kinase.";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
 CC "FUNCTION: INVOLVED IN THE ACTIVATION OF A MEIOTIC GENES ACTIVATION
 CC PATHWAY."
 CC "PTM: AUTOPHOSPHORYLATED."
 CC "SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
 CC PROTEIN KINASES. STRONG, WITH S.POMBE CTK1."
 CC
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 CC
 DR EMBL; D50617; BAA09206.1; -.
 DR EMBL; U83459; AAB6408.1; -.
 DR EMBL; AJ001030; CAA04486.1; -.
 DR FSSP; Q63450; 1A06;
 DR SGD; S0001861; RIM15;
 DR InterPro; IPR000719; -.
 DR InterPro; IPR001789; -.

DR InterPro: IPR002290; -.
 DR Pfam: PF00069; Pkinase; 2.
 DR Pfam: PF00072; response_reg; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_SP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Phosphotransferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphotransferase; Melotose; -.
 FT DOMAIN 343 358 POLY ASN.
 FT DOMAIN 620 624 POLY SER.
 FT DOMAIN 794 1254 PROTEIN KINASE.
 FT NP_BIND 800 808 ATP (BY SIMILARITY).
 FT BINDING 823 823 ATP (BY SIMILARITY).
 FT ACT_SITE 918 918 BY SIMILARITY.
 FT DOMAIN 975 980 POLY ASN.
 FT DOMAIN 1213 1218 POLY SLU.
 FT DOMAIN 1386 1391 POLY THR.
 SQ SEQUENCE 1770 AA; 196530 MW; DC1064825000FAFF CRC64; 1

Query Match 73.38; Score 33; DB 1; Length 1770;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLE 8 DR 272 LHNDNLE 279

RESULT 13
 ID RLAL_CHLRE STANDARD PRT; 107 AA.
 AC P29763.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-JUL-1993 (Rel. 25, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 605 ACIDIC RIBOSOMAL PROTEIN P1.
 OS Chlamydomonas reinhardtiae.
 OC Chlamydomonadaceae; Chlamydomonas.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=137C;
 DR Dumont F.;
 RL Submitted (MAY 1992) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
 PROTEIN SYNTHESIS (BY SIMILARITY).
 CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
 CC SUBUNIT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
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 DR EMBL: X66411; CAA47042.1; -.
 DR PIR: S24990; R6RMIC.
 DR InterPro: IPR01813; -.
 DR Pfam: PF000428; 60S_ribosomal; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 107 AA; 10875 MW; 2A7FC9696D8617BF CRC64; 1

Query Match 71.18; Score 32; DB 1; Length 107;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLE 8

DR 14 ILHDDOLE 11

RESULT 14
 ID YVAE_VACCC STANDARD PRT; 166 AA.
 AC P20514;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE HYPOTHETICAL 18.2 KDa PROTEIN.
 GN A ORF E.
 OS Vaccinia virus (strain Copenhagen).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TAXID=10249;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91021027; PubMed=2219722;
 RA Goebel S.J.; Johnson G.P.; Perkus M.E.; Davis S.W.; Winslow J.P.,
 RA Paolletti E.;
 RT The complete DNA sequence of vaccinia virus.";
 RL Virology 179:247-266 (1990).
 RN [12]
 RP COMPLETE GENOME.
 RA Goebel S.J.; Johnson G.P.; Perkus M.E.; Davis S.W.; Winslow J.P.,
 RA Paolletti E.;
 RL Virology 179:517-563 (1990).
 CC

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Query Match 71.18; Score 32; DB 1; Length 166;
 Best Local Similarity 55.6%; Pred. No. 20;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLEA 9 DR A42524; A42524;
 KW Hypothetical protein.
 SQ SEQUENCE 166 AA; 18230 MW; 5927A96A0CB9477B CRC64;

RESULT 15
 ID BZLF_EBV STANDARD PRT; 245 AA.
 AC P03206;
 DT 01-JUL-1996 (Rel. 01, Created)
 DT 01-MAR-1999 (Rel. 10, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE BZLF1_TRANS_ACTIVATOR_PROTEIN (EB1) (ZEBRA).
 GN BZLF1.
 OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammapathovirinae; Lymphocryptovirus.
 NCBI_TAXID=10377;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84210667; PubMed=6087149;
 RA Baer R.; Bannier A.T.; Biggin M.D.; Deininger P.L.; Farrell P.J.,
 RA Gibson T.J.; Hatfull G.; Hudson G.S.; Satchwell S.C.; Seguin C.,
 RA Tuffnell P.S.; Barrell B.G.;
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";

RL RN Nature 310:207-211(1984).
 [2] RP IDENTIFICATION OF PROTEIN.
 RX MEDLINE=87311873; PubMed=3041034;
 RA Farrel P.J., Rowe D.T., Rooney C.M., Kouzarides T.;
 RT "Epstein-Barr virus BZLF1-trans-activator specifically binds to a
 consensus AP-1 site and is related to c-fos.";
 RT cells.";
 RT cells.";
 RL RN J. Virol. 61:3120-3132(1987).
 [3] RP DNA-BINDING.
 RX MEDLINE=89231610; PubMed=2540954;
 RA Farrel P.J., Rowe D.T., Rooney C.M., Kouzarides T.;
 RT "Epstein-Barr virus BZLF1-trans-activator specifically binds to a
 consensus AP-1 site and is related to c-fos.";

RL RN [4] RT EMBO J. 8:127-132(1989).
 RP STRUCTURE, AND FUNCTION.
 RX MEDLINE=90219210; PubMed=2157874;
 RA Packiam G., Economou A., Rooney C.M., Rowe D.T., Farrel P.J.;
 RT "Structure and function of the Epstein-Barr virus BZLF1 protein.";
 RL J. Virol. 64:2110-2116(1990).
 RN [5] RP FUNCTION.
 RX MEDLINE=94008999; PubMed=8404860;
 RA Scheers A., Pich D., Hammerichmidt W.;
 RT "A transcription factor with homology to the AP-1 family links RNA
 transcription and DNA replication in the lytic cycle of Epstein-Barr
 virus.";
 RL EMBO J. 12:3921-3929(1993).
 CC -1- FUNCTION: BZLF1 PLAYS A KEY ROLE IN THE SWITCH FROM LATENT TO
 CC PRODUCTIVE INFECTION OF EBV. BZLF1 ACTIVATES THE PROMOTER OF AN
 CC OTHER EBV GENE (BSL2+BMF1).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.

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 CC
 DR EMBL; V01555; CAA24861.1; -.
 PIR; A03768; Q0BE27.
 DR PIR; S03634; S03634.
 DR TRANSPAC; T00933; -.
 DR Interpro; IPR01871; -.
 DR Pfam; PF00170; b2IP; 1.
 DR PROSITE; PS00036; BZIP_BASIC; 1.
 KW transcription regulation; DNA-binding; Nuclear protein; Early protein.
 FT DNA_BIND 178 195 BASIC MOTIF.
 SQ SEQUENCE 245 AA; 26860 MW; 7F5D55D79F1F0196 CRC64;

Query Match Score 32; DB 1; Length 245;
 Best Local Similarity 71.1%; Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VLHDDLL 7
 Db 237 VLHEDLL 243

RESULT 2		"Panton-valentine leukocidin genes in a phage-like particle isolated from mitomycin C-treated <i>Staphylococcus aureus</i> V8 (ATCC 49775).";
ID Q92619; AC Q92619; DT 01-FEB-1997 (TREMBLrel. 02, Created); DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	PRT; 1165 AA.	RT RT Biosci. Biotechnol. Biochem. 61:1960-1962 (1997). EMBL; AB009866; BAA1891-1; -; SEQUENCE 119 AA; 13921 MW; OF2A472DB7D63FA0 CRC64;
DE MYELOBLAST KIAA0223 (FRAGMENT).		
GN KIAA0223.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX NCBI_TAXID=9606; (1)		
RN RP SEQUENCE FROM N.A.		
RC TISSUE-BONE MARROW; MEDLINE=97191544; PubMed=9039502;		
RX RA Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; "Prediction of the coding sequences of unidentified human genes. VI. the coding sequences of 80 new genes (KIAA0201-KIAA0288) deduced by analysis of cDNA clones from cell line KG-1 and brain.", DNA Res. 3:321-329(1996).	PRT; 1165 AA.	RT RT (TREMBLrel. 15, Created) RT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) RT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
RN RP SEQUENCE OF 170-1165 FROM N.A.		
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S., Phan H., Velasco N., Garnes J., Daugan L., Poundstone P., Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G., Copefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Klemmiller B., Arellano M., Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O., Carrano A.V.; Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.	PRT; 496 AA.	RT RT (TREMBLrel. 15, Created) RT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) RT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
RL EMBL; D86916; BAA1322.1; -.		DE PHI_PVL ORF 18 AND 19 HOMOLOGUE. RT
DR EMBL; AC004151; AAC03237.1; -.		OS <i>Staphylococcus aureus</i> strain P83." RT
DR HSSP; Q07960; IKGSP.		RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases. RT
DR InterPro; IPR00198; -.		RN Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases. RN
DR InterPro; IPR002119; -.		RC STRAIN=P83; SEQUENCE FROM N.A.
DR pfam; PF00130; DAG_PE-bind; 1.		RX MEDLINE=98067870; PubMed=9404084;
DR pfam; PF00630; RhogAP; 1.		RA Raneko J., Muramoto K., Kamio Y.; Gene of LukF-PV-like component of Panton-Valentine leukocidin in <i>Staphylococcus aureus</i> P83 is linked with LukM."
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.		RT RT DR EMBL; AB044554; BAA7859.1; -.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.		SQ SEQUENCE 496 AA; 56878 MW; 1BEE4F6E697920584 CRC64;
DR SMART; SM00324; RhogAP; 1.		
FT NON_TER 1 1		
FT SEQUENCE 1165 AA; 12734 MW; 92EF768CAF0458C9 CRC64;		
Query Match Best Local Similarity 82.28%; Score 37; DB 4; Length 1165; Matches 8; Conservative 8; Indels 0; Gaps 0;	PRT; 1165 AA.	Query Match Best Local Similarity 85.78%; Score 35; DB 9; Length 496; Matches 6; Conservative 6; Indels 0; Gaps 0;
Qy 1 VLHDDLEA 9		Qy 3 HDDILEA 9
Db 166 VLRRDDEA 174		Db 72 HDDILEA 78
RESULT 3		RESULT 5
080057	PRELIMINARY;	027025 PRELIMINARY;
ID 080057	PRT; 119 AA.	ID 027025 PRT; 616 AA.
AC 080057;		AC 027025
DT 01-NOV-1998 (TREMBLrel. 08, Created)		DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)		DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE ORF 18.		DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
OS bacteriophage phi PVL.		DE TYPE I RESTRICTION MODIFICATION ENZYME, SUBUNIT M.
OC Viruses.		GN MTH942.
OX NCBI_TAXID=71366;		OS Methanobacterium thermoautotrophicum.
RN (1)		OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
RP SEQUENCE FROM N.A.		OC Methanothermobacteria.
RX MEDLINE=98067870; PubMed=9404084;		OX NCBI_TAXID=145262;
RA Kaneko J., Kimura T., Kawakami Y., Tomita T., Kamio Y.;		RN SEQUENCE FROM N.A.
RX MEDLINE=98037514; PubMed=9371463;		RC STRAIN=DELTIA H.
RX MEDLINE=98037514; PubMed=9371463;		RX

PROSITE; PS01114; GPR1_FUN34_YAAH; 1.	Query Match	81.0%	Score	34	DB	1	Length	343
TRANSMEM	POTENTIAL.	107	POTENTIAL.					
TRANSMEM	POTENTIAL.	120	POTENTIAL.					
TRANSMEM	POTENTIAL.	151	POTENTIAL.					
TRANSMEM	POTENTIAL.	185	POTENTIAL.					
TRANSMEM	POTENTIAL.	208	POTENTIAL.					
TRANSMEM	POTENTIAL.	239	POTENTIAL.					
SEQUENCE	282 AA;	30701 MW;	F5E20F9324CEB8199	CRC64;				
RESULT	2	81.0%	Score	34	DB	1	Length	282;
Best Local Matches	7;	Similarity	87.5%;	Pred.	No.	12;		
0;	Mismatches	1;	Indels	0;	Gaps	0;		
2	LRDDLEA	9						
1 1 1 1 1								
62	LRDDLEA	69						
RESULT	2	81.0%	Score	34	DB	1	Length	282;
Best Local Matches	7;	Similarity	87.5%;	Pred.	No.	12;		
0;	Mismatches	1;	Indels	0;	Gaps	0;		
2	LRDDLEA	9						
1 1 1 1 1								
62	LRDDLEA	69						
RESULT	3	81.0%	Score	34	DB	1	Length	343;
Best Local Matches	7;	Similarity	87.5%;	Pred.	No.	15;		
1;	Mismatches	1;	Indels	0;	Gaps	0;		
QY	1	VLRDDLEA	9					
1 1 1 1 1								
DB	238	VRDDLEA	246					
RESULT	3	81.0%	Score	34	DB	1	Length	343;
Best Local Matches	7;	Similarity	87.5%;	Pred.	No.	15;		
1;	Mismatches	1;	Indels	0;	Gaps	0;		
ID	OL56_STRAT		STANDARD:					
AC	Q07017							
DT	01-NOV-1997	(Rel.	35	Created)				
DT	01-NOV-1997	(Rel.	35	Last sequence update)				
DT	15-JUL-1999	(Rel.	38	Last annotation update)				
DE	OLEANDROMYCIN POLYKETIDE SINTHASE, MODULES 5 AND 6.							
GN	ORFB.							
OS	Streptomyces antibioticus.							
OC	Bacteria; Firmicutes; Actinobacteria; Streptomyctaceae; Streptomyces.							
NCBI_TaxID=1890;								
RN	(1)							
RP	SEQUENCE FROM N.A.							
RX	MEDLINE=94150470; PubMed=9107683;							
RA	Swan D.G., Rodriguez A.M., Vilches C., Mendez C., Salas J.A.;							
RT	"Characterisation of a Streptomyces antibioticus gene encoding a type I Polyketide Synthase which has an unusual coding sequence."							
RL	Mol. Gen. Genet. 242:358-362 (1994).							
CC	-1. FUNCTION: MAY BE INVOLVED IN THE BIOSYNTHESIS OF THE OLEANDROMYCIN							
CC	LACTONE RING.							
CC	-1. COFACTOR: CONTAINS 1 COVALENTLY BOUND PHOSPHOPANTETHINE (FAS)							
CC	-1. SIMILARITY: TO FATTY ACID SYNTHASE (FAS)							
CC	-----							
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CC	CC	SEQUENCE FROM N.A.						
STRAIN=JAL-1 / DSM 2661 / ATCC 42067;								
MEDLINE=9537959; PubMed=8686087;								
Built C.-J. White O., Olsen G.J., Zhou L., Fleischmann R.D., Kerlavage A.R., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Dougherty B.A., Tomb J.F., Weinstock G.F., Adams M.D., Reich C.I., Overbeek R., Kirchner E.F., Weissenbach J.M., Mekrrik J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadovskaya N.M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."								
Science 273:1058-1073 (1996).								
+ NAD(+)	= 1,3-DIPHOSPHATEGLYCERATE + NADH.							
-!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE								
-!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.								
-!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).								
-!- SUBCELLULAR LOCATION: CYTOSOLIC.								
-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.								
CC	-----							
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EMBL; U67557; AAB99147.1;	-							
TIGR; MJ1146;								
InterPro; IPR00173;	-							
Pfam; PF00044; gpdh; 1.								
PROSITE; PS00071; GAPDH; 1.								
Glycyls; Oxidoreductase;	NAD;							
BINDING; 144	GLYCERALDEHYDE 3-PHOSPHATE (BY SIMILARITY).							
SEQUENCE	343 AA;	38102 MW;	81E5810A9C81BC5	CRC64;				

FT	ACT_SITE	660	660	ACYL ENZYME INTERMEDIATE.		SQ	SEQUENCE	465 AA;	51606 MW;	019A80B3B25957EF CRC64;
FT	NP_BIND	1203	1249	NADP.						
FT	BINDING	1524	1524	PHOSPHOPANTETHINE (BY SIMILARITY).						
FT	ACT_SITE	1859	1859	BETA KETOACYL SYNTHASE.						
FT	ACT_SITE	2311	2311	ACYL ENZYME INTERMEDIATE.						
FT	NP_BIND	2859	2905	NADP.						
FT	BINDING	3178	3178	PHOSPHOPANTETHINE (BY SIMILARITY).						
SQ	SEQUENCE	3519	AA;	368361 MW;	41AE78AAE61F6 CRC64;					
Query	Match	81.0%		Score 34;	DB 1;	Length 3519;				
Best	Local	Similarity	87.5%	Pred. No. 1.9e+02;						
Matches	7;	Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;				
Qy	2	LRDDLIE	9				RESULT 5			
Db	770	LRDELLER	777				EPS8_HUMAN	STANDARD;	PRT;	822 AA.
RESULT 4							ID	EPS8_HUMAN		
RBL_DAPS							AC	012929;		
ID	P28397						DT	01-NOV-1997 (Rel. 35, Created)		
AC							DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)						DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)						DE	EPITDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPSS.		
DT	01-OCT-2000 (Rel. 40, Last annotation update)						DE			
DE	RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO DE LARGE SUBUNIT) (FRAGMENT).						GN			
GN	RBC1.						EPS8.			
OS	Chloroplast; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Daphniphyllum sp.						OS	Homo sapiens (Human).		
OC	Magnoliophyta; eudicots; core eudicots; Daphniphyllum.						OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.		
OX	NCBI_TaxID:4388;						OX	NCBI_TaxID:9606;		
RP	SEQUENCE FROM N.A.						RN			
RX	Albert V.A., Williams S.E., Chase M.W.; RT						RP	SEQUENCE FROM N.A.		
RA	RT Carnivorous Plants: Phylogeny and structural evolution. ; RT Science 257:1491-1495 (1992).						RA	MEDLINE=94166756; PubMed=8084614;		
RL	CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE.						RA	Wong W.T., Carliomagno F., Druck T., Barletta C., Croce C.M., Hebbner K., Kraus M.H., di Fiore P.P.; RT		
CC	CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2,3-PHOSPHO-D-GLYCERATE.						RA	"Evolutionary conservation of the EPSS gene and its mapping to human chromosome 12q23-q24."		
CC	CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.						RT	ONCogene 9;3057-3061(1994); CC -1- FUNCTION: UPON BINDING TO EGFR RECEPTOR ENHANCES EGF-DEPENDENT MITOGENIC SIGNALS. CAN BIND MULTIPLE CELLULAR TARGETS.		
CC	CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.						CC	CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES ANALYZED, INCLUDING HEART, BRAIN, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY AND PANCREAS. EXPRESSED IN ALL EPITHELIAL AND FIBROBLASTIC LINES EXAMINED. AND IN SOME, BUT NOT ALL, HEMATOPOIETIC CELLS.		
CC	CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.						CC	CC -1- PH: PHOSPHORYLATED BY SEVERAL RECEPTOR TYROSINE KINASES.		
CC	CC -1- SIMILARITY: CONTAINS 1 SPLIT PH DOMAIN.						CC	CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.		
CC	CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).						CC	CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	CC -1- DR HSSP: P00875; IRAO.						CC	CC -1- DR HSSP: P00875; IRAO.		
CC	CC -1- DR InterPro: IPR00085;						CC	CC -1- DR InterPro: IPR001452;		
CC	CC -1- DR Pfam: PF00016;						CC	CC -1- DR Pfam: PF00018; SH3; 1.		
CC	CC -1- DR PROSITE: PS00022; SH3; 1.						CC	CC -1- DR PROSITE: PS00022; SH3; 1.		
CC	CC -1- DR SH3 domain; Phosphorylation. PH (FIRST PART).						CC	CC -1- DR SH3 domain; Phosphorylation. PH (FIRST PART).		
CC	CC -1- DR DOMAIN: 69 129 PH (FIRST PART).						CC	CC -1- DR DOMAIN: 69 129 PH (FIRST PART).		
CC	CC -1- DR DOMAIN: 210 213 POLY-PH0.						CC	CC -1- DR DOMAIN: 210 213 POLY-PH0.		
CC	CC -1- DR DOMAIN: 322 325 POLY-PH0.						CC	CC -1- DR DOMAIN: 322 325 POLY-PH0.		
CC	CC -1- DR DOMAIN: 381 414 PH (SECOND PART).						CC	CC -1- DR DOMAIN: 381 414 PH (SECOND PART).		
CC	CC -1- DR DOMAIN: 421 440 PRO-RICH.						CC	CC -1- DR DOMAIN: 421 440 PRO-RICH.		
CC	CC -1- DR DOMAIN: 532 591 PRO-RICH.						CC	CC -1- DR DOMAIN: 532 591 PRO-RICH.		
CC	CC -1- DR DOMAIN: 615 651 PRO-RICH.						CC	CC -1- DR DOMAIN: 615 651 PRO-RICH.		
CC	CC -1- DR DOMAIN: 659 664 POLY-SER.						CC	CC -1- DR DOMAIN: 659 664 POLY-SER.		
CC	CC -1- DR SEQUENCE 822 AA; 91881 MW; AC5EB1D2B8784B3B CRC64;						CC	CC -1- DR SEQUENCE 822 AA; 91881 MW; AC5EB1D2B8784B3B CRC64;		
CC	CC -1- DR Similarity 78.6%; Score 33; DB 1; Length 822;						CC	CC -1- DR Similarity 78.6%; Score 33; DB 1; Length 822;		
CC	CC -1- DR Mismatches 0; Indels 0; Gaps 0;						CC	CC -1- DR Mismatches 0; Indels 0; Gaps 0;		

Qy 1 VLRDDLE 8
 Db 552 VLKDILE 559

RESULT 6
 SYL_MYCTD STANDARD; PRT; 1041 AA.

AC Q10765; 006181;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 15-DEC-1996 (Rel. 37, Last annotation update)
 DE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE)

OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacteriaceae; Mycobacterium.

NCBI_TaxID=1769;
 RN [1]

RP SEQUENCE FROM N.A.

RC Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinomycetales; Corynebacteriaceae; Mycobacterium.

NCBI_TaxID=1773;
 RN [1]

RP STRAIN=H77RV; PubMed=9634230;

RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglemeier K., Barry C.E. III, Teklaia F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jageis K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Skelton S., Squares S., Squares R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.",
 RL Nature 393:537-544(1998).

CC -1- CATALYTIC ACTIVITY: ATP + L-ISOLEUCINE + TRNA(ILE) = AMP +
 CC PYROPHOSPHATE + L-ISOLEUCYL TRNA(ILE).

CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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CC EMBL; 774020; CAA98326.1; -.

DR InterPro; Rv1526; -.

DR InterPro; IPR01412; -.

DR InterPro; IPR002300; -.

DR InterPro; IPR002301; -.

DR Pfam; PF00133; TRNA-synth_1; 1.

DR PRINTS; PS00584; TRNA-SYNTHE.

DR PROSITE; PS00178; AA-TRNA-LIGASE_I; 1.

KW Aminocyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Metal-binding; Zinc.

FT SITE 53 63 "HIGH" REGION.
 FT SITE 61 9 623 "KMSKS" REGION.
 FT BINGING 622 622 ATP (BY SIMILARITY).
 SQ SEQUENCE 1041 AA; 117339 MW; B5023822848808C6 CRC64;

Query Match 78.6%; Score 33; DB 1; Length 1041;
 Best Local Similarity 77.8%; Pred. No. 78; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLE 9
 Db 710 VLRDDLES 718

RESULT 7
 SYL_MYCLE STANDARD; PRT; 1059 AA.

AC Q9X7E5;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE)

GN TILES OR MLCH458 10.

OS Mycobacterium leprae.

OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacteriaceae; Mycobacterium.

NCBI_TaxID=1769;
 RN [1]

RP SEQUENCE FROM N.A.

RA Seeger K.J., Harris D., James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RA Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 RL -1- CATALYTIC ACTIVITY: ATP + L-ISOLEUCINE + TRNA(ILE) = AMP +
 CC PYROPHOSPHATE + L-ISOLEUCYL TRNA(ILE).
 CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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CC DR AL049478; CAB30575.1; -.

DR InterPro; IPR002300; -.

DR InterPro; IPR002311; -.

DR Pfam; PF00133; TRNA-synth_1; 1.

DR PRINTS; PRO0984; TRNA-SYNTHE.

DR PROSITE; PS00178; AA-TRNA-LIGASE_I; 1.

KW Aminocyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

KW Metal-binding; Zinc.

FT SITE 59 69 "HIGH" REGION.
 FT SITE 637 641 "KMSKS" REGION.

FT BINDING 640 640 ATP (BY SIMILARITY).

SQ SEQUENCE 1059 AA; 119808 MW; 67FC7659E9399E39 CRC64;

Query Match 78.6%; Score 33; DB 1; Length 1059;
 Best Local Similarity 77.8%; Pred. No. 79; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLEA 9
 Db 728 VLRDDLSQA 736

RESULT 8
 YCV5_SCHPO STANDARD; PRT; 264 AA.

AC Q13679;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL 30.7 KDA PROTEIN C737.05 IN CHROMOSOME III.

GN SPC737.05.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomyces.

OC Schizosaccharomyces.

NCBI_TaxID=4896;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Murphy L., Harris D., Wood V., Lyne M.H., Rajandream M.A.,
 RA Barrell B.G.; EMBL/GenBank/DBJ databases.
 RL Submitted (SBP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

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 CC

DR EMBL; AL031546; CAB44773.1; -.

KW Hypothetical protein; Transmembrane.

FT 48 POTENTIAL.

FT TRANSMEM 112 132

FT TRANSMEM 142 162 POTENTIAL.

SEQUENCE 264 AA; 30665 MW; D0EE75C409F09F0B CRC64;

Query Match 76.28; Score 32; DB 1; Length 264;
 Best Local Similarity 55.68; Pred. No. 27; Gaps 0;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDDLE 9
 Db 26 IIRDELVA 34

RESULT 9
 NA37_ECOLI STANDARD; PRT; 334 AA.
 ID NA37_ECOLI
 AC P31970;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 37 KDA NUCLEOID-ASSOCIATED PROTEIN.
 GN YEJK.

OS Escherichia coli.

OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TAXID=512;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=K12 / BHB7600;

RA Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
 RA Church G.M., Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE-97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [3]

RP SEQUENCE OF 1-15.

RX MEDLINE-9929598; PubMed=10368163;

RA Murphy L.D., Rosner J.L., Zimmerman S.B., Esposito D.;
 RT "Identification of two new proteins in spermidine nucleoids isolated
 RL J. Bacteriol. 181:3842-3844(1999).

CC -1 FUNCTION: NOT KNOWN.

CC -1 SUBCELLULAR LOCATION: SEEMS TO BE ASSOCIATED WITH THE NUCLEOID.

CC -1 SIMILARITY: STRONG, TO H. INFLUENZAE H10839.

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 CC

Trochodendron aralioides.
 OS "Genome sequences of *Chlamydia trachomatis* MoPh and *Chlamydia pneumoniae* AR39";
 RT RT
 RT Nucleic Acids Res. 28:1397-1406 (2000).
 RL [3]
 RN SEQUENCE FROM N.A.
 STRAIN=J13B
 RC MEDLINE=20330349; PubMed=10871362;
 RX RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kubara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of *Chlamydia pneumoniae* J13B
 RT from Japan and CWL029 from USA";
 RL Nucleic Acids Res. 28:2311-2314 (2000).
 CC -1- FUNCTION: PRESUMABLY INVOLVED IN THE PROCESSING AND REGULAR
 CC -1- TURNOVER OF INTRACELLULAR PROTEINS. CATALYZES THE REMOVAL OF
 CC -1- UNSUBSTITUTED AMINO-TERMINAL AMINO ACIDS FROM VARIOUS PEPTIDES (BY
 CC -1- SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: RELEASE OF AN N-TERMINAL AMINO ACID, XAA [-
 CC -1- XBB -], IN WHICH XAA IS PREFERABLY LEU, BUT MAY BE OTHER AMINO ACIDS
 CC -1- INCLUDING PRO ALTHOUGH NOT ARG OR LYS, AND XBB MAY BE PRO.
 CC -1- COFACTOR: MANGANESE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1; ALSO KNOWN AS THE
 CC -1- CYTOSOL AMINOPEPTIDASE.
 CC -1- CYTOSOL AMINOPEPTIDASE FAMILY.
 CC -1-
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 CC -1-
 DR EMBL; AE001623; PADI0529_1;
 DR HSSP; P00876; 3RUB.
 DR Mendel; 2879; TRoar; rbcL_1.
 DR InterPro; IPI000085;
 DR Pfam; PF00016; RUBISCO_LARGE; 1.
 DR PROSITE; PS00157; RUBISCO_LARGE; 1.
 KW Photosynthesis; Carbon dioxide fixation; Photorespiration;
 KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast.
 FT ACT_SITE 191 1 BINDING OF CO(2) ACTIVATES THE ENZYME.
 FT ACT_SITE 191 1
 SQ SEQUENCE 465 AA; 51691 MW; ED085903CCF3BBAD CRC64;
 SQ
 Query Match Score 32; DB 1; Length 465;
 Best Local Similarity 75.0%; Pred. No. 51; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 2;
 Db 338_LLRDLDVE 345
 QY 1 VLRDLDLE 8
 Db 338_LLRDLDVE 345
 RESULT 14
 AMPA_CHLPN STANDARD; PRT; 499 AA.
 ID AMPA_CHLPN
 AC Q9Z88; Q9JQ12;
 AC Q9Z88; Q9JQ12;
 DR 30-MAY-2000 (Rel. 39, Created)
 DR 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTIDASE)
 DE (LAP) (LEUCYL AMINOPEPTIDASE).
 GN PEP-A OR CPN0385 OR CP0370.
 OS *Chlamydia pneumoniae* (Chlamydophila pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 RX "Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*."
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHLO29;
 RX MEDLINE=9920606; PubMed=10192388;
 RA Kalman S., Mitchell R., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinske L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*."
 RL Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwyn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RA

Query Match Score 32; DB 1; Length 499;
 Best Local Similarity 77.8%; Pred. No. 55; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 1;
 QY 1 VLRDLDLEA 9
 Db 395_VLAEDLEA 403
 RESULT 15
 CYSJ_ECOLI STANDARD; PRT; 598 AA.
 ID CYSJ_ECOLI
 AC P38038; P14782;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SULFITE REDUCTASE [NADPH] FLAVOPROTEIN ALPHA-COMPONENT (EC 1.8.1.2)
 DE (S-TR-FP).
 CN CYSJ.
 OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia;
 OC Escherichia;
 OC Escherichia;
 OC Escherichia;
 OX NCBI_TAXID=562;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=N.B;
 RX MEDLINE=89380164; PubMed=2550423;
 RA Ostrowski J., Barber M.J., Rueger D.C., Miller B.E., Siegel L.M.,
 RA Kredich N.M.;
 RT "Characterization of the flavoprotein moieties of NADPH-sulfite
 reductase from *Salmonella typhimurium* and *Escherichia coli*.
 RT Physicochemical and catalytic properties, amino acid sequence deduced
 RT from DNA sequence of *cysJ*, and comparison with NADPH-cytochrome P-450
 RT reductase.";
 RL J. Biol. Chem. 264:15795-15808(1989).
 [2] RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Coliaco-Vides J., Glashier J.D., Rode C.K., Maynew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474 (1997).
 RN [3] SEQUENCE OF 593-598 FROM N.A.
 RP STRAIN=N.B;
 RX MEDLINE=89359425; PubMed=2670946;
 RA Ostrowski J., Wu J.-Y., Rueger D.C., Miller B.E., Siegel L.M.,
 RA Kredich N.M.;
 RT "Characterization of the CYSJTH regions of *Salmonella typhimurium* and
 RT *Escherichia coli*. DNA sequences of *cysJ* and *cysH* and a model for
 RT the *Escherichia coli*-*cysS4* active center of sulfate reductase hemoprotein
 RT based on amino acid homology with spinach nitrite reductase.";
 RL J. Biol. Chem. 264:15726-15737(1989).
 CC -1: FUNCTION: THIS ENZYME CATALYZES THE 6-ELECTRON REDUCTION OF
 CC SULFITE TO SULFIDE. THIS IS ONE OF SEVERAL ACTIVITIES REQUIRED
 CC FOR THE BIOSYNTHESIS OF L-CYSTEINE FROM SULFATE. THE FLAVO-
 PROTEIN COMPONENT CATALYZES THE ELECTRON FLOW FROM NADPH ->
 CC FAD -> FMN TO THE HEMOPROTEIN COMPONENT. THE FLAVO-
 CC -1: CATALYTIC ACTIVITY: HYDROGEN SULFIDE + 3 NADP(+) + 3 H(2)O =
 CC SULFITE + 3 NADPH.
 CC -1: COFACTOR: THIS SUBUNIT IS A FLAVOPROTEIN THAT BINDS ONE FMN AND
 CC ONE FAD PER CHAIN.
 CC -1: SUBUNIT: ALPHA(8)-BETA(4). THE ALPHA COMPONENT IS A FLAVOPROTEIN,
 CC THE BETA COMPONENT IS A HEMOPROTEIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions. This statement is not removed, usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch).
 CC
 EMBL; M23008; AAA23650.1; -.
 DR EMBL; U29579; AAA69274.1; -.
 DR EMBL; AE000360; AAC758006.1; -.
 DR P18; B34231; B34231.
 DR HS3P; P00388; IAMO.
 DR EcGene; EG10191; cysJ.
 DR InterPro; IPR001094; -.
 DR InterPro; IPR001433; -.
 DR InterPro; IPR001709; -.
 DR InterPro; IPR003097; -.
 DR Pfam; PF00567; FAD_binding_1.
 DR Pfam; PF00175; Oxidored_fad; 1.
 DR PRINTS; PRO0369; FLAVODOXIN.
 DR PRINTS; PRO0371; FPMCR.
 KW Oxidoreductase; Flavoprotein; NADP; FAD; FMN; Electron transport
 KW Cysteine biosynthesis.
 KW INIT_MET. 0 0

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2001, 08:32:06 ; Search time 18:74 Seconds
(without alignments)
9.675 Million cell updates/sec

title: US-09-489-760-5

perfect score: 42
Sequence: 1 VIRDDEEA 9

Scoring table: BLOSUM62
Gapext 0.5

Scanned: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA: *
1: /cgns2_6/picodata/2/1aa/5A.COMB.pep: *
2: /cgns2_6/picodata/2/1aa/5B.COMB.pep: *
3: /cgns2_6/picodata/2/1aa/6A.COMB.pep: *
4: /cgns2_6/picodata/2/1aa/6B.COMB.pep: *
5: /cgns2_6/picodata/2/1aa/PCUTS.COMB.pep: *
6: /cgns2_6/picodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	33	78.6	1045	1	US-08-552-083-2		Sequence 2, Appli
2	31	73.8	251	5	PCU-US95-1257A-1		Sequence 1, Appli
3	31	73.8	508	2	US-08-561-664-10		Sequence 10, Appli
4	31	73.8	508	2	US-08-596-001-10		Sequence 10, Appli
5	31	73.8	508	4	US-09-433-433A-10		Sequence 10, Appli
6	31	73.8	599	3	US-08-556-419-22		Sequence 22, Appli
7	31	73.8	629	3	US-08-556-419-23		Sequence 23, Appli
8	31	73.8	2509	1	US-08-169-005A-10		Sequence 10, Appli
9	30	71.4	483	2	US-08-770-544-8		Sequence 8, Appli
10	30	71.4	821	1	US-07-335-311A-4		Sequence 4, Appli
11	30	71.4	821	1	US-08-368-079-4		Sequence 4, Appli
12	30	71.4	821	5	PCU-US95-07956-4		Sequence 4, Appli
13	30	71.4	1159	2	US-08-936-242-13		Sequence 13, Appli
14	30	71.4	1159	3	US-09-351-215-13		Sequence 13, Appli
15	30	71.4	1159	4	US-09-226-012-2		Sequence 2, Appli
16	29	69.0	1159	4	US-09-226-012-4		Sequence 4, Appli
17	29	69.0	283	2	US-08-701-191A-41		Sequence 41, Appli
18	29	69.0	790	1	US-08-363-580-2		Sequence 2, Appli
19	29	69.0	1410	4	US-09-335-409-3		Sequence 3, Appli
20	29	69.0	2165	1	US-08-514-975B-2		Sequence 2, Appli
21	29	69.0	2165	5	PCU-US95-12507-2		Sequence 2, Appli
22	29	69.0	2713	5	PCU-US95-01735-1		Sequence 1, Appli
23	28	66.7	240	1	US-07-965-666A-3		Sequence 3, Appli
24	28	66.7	240	2	US-08-950-433-3		Sequence 3, Appli
25	28	66.7	245	4	US-08-394-483-69		Sequence 69, Appli
26	28	66.7	275	2	US-09-016-366A-17		Sequence 17, Appli

ALIGNMENTS							
28	28	66.7	275	2	US-08-978-404B-12	Sequence 12, Appli	
29	28	66.7	649	2	US-08-871-366B-16	Sequence 16, Appli	
30	28	66.7	649	3	US-09-018-864A-16	Sequence 22, Appli	
31	28	66.7	1832	4	US-08-871-267B-22	Sequence 4, Appli	
32	28	66.7	7257	4	US-09-335-409-4	Sequence 5, Appli	
33	28	66.7	7257	4	US-09-217-609A-11	Sequence 11, Appli	
34	27	64.3	9	3	US-08-217-609A-11	Sequence 11, Appli	
35	27	64.3	9	4	US-08-873-235B-11	Sequence 8, Appli	
36	27	64.3	120	2	US-08-232-887A-8	Sequence 7, Appli	
37	27	64.3	122	2	US-08-232-887A-7	Sequence 5, Appli	
38	27	64.3	139	1	US-08-469-592-5	Sequence 6, Appli	
39	27	64.3	140	1	US-07-846-592-6	Sequence 4, Appli	
40	27	64.3	140	1	US-07-846-592-6	Sequence 4, Appli	
41	27	64.3	140	1	US-07-846-592-6	Sequence 4, Appli	
42	27	64.3	140	1	US-08-169-555-4	Sequence 6, Appli	
43	27	64.3	200	1	US-08-169-555-6	Sequence 6, Appli	
44	27	64.3	200	1	US-07-855-112B-1	Sequence 1, Appli	
45	27	64.3	200	2	US-08-308-887A-1	Sequence 1, Appli	

RESULT 1
US-08-452-083-2
; Sequence 2, Application US/08452083
; Patent No. 5756327
; GENERAL INFORMATION:
; APPLICANT: Sasseanfar, Mandana
; SCHIMMEL, Paul R.
; TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL ISOLEUCYL-tRNA
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; STREET: Two Millita Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,083
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/305,765
; FILING DATE: 13-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOK, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CP194-08B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6440
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1045 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-452-083-2

Query Match Similarity 78.6%; Score 33; DB 1; Length 1045;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLRDDEA 9

RESULT ²
 PCT-US95-12357A-1
 ; Sequence 1, Application PC/TUSS9512357A
 ; GENERAL INFORMATION:
 ; APPLICANT: St. Jude Children's Research Hospital
 ; TITLE OF INVENTION: Nucleic Acid Encoding Mutant Matrix
 ; PROTEINS Useful for Attenuation or Enhancement of
 ; INFLUENZA A Virus, Vaccines and Methods of making and
 ; using Thereof
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STEINE, KESSLER, GOLDSTEIN & FOX
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/12357A
 ; FILING DATE: 29-SEPT-1995
 ; CLASSIFICATION:
 ; PRIORITY NUMBER: 08/316,419
 ; FILING DATE: 30-SEPT-1994
 ; CLASSIFICATION:
 ; APPLICATION NUMBER: 08/471,100
 ; FILING DATE: 6-JUNE-1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fox, Samuel L.
 ; REGISTRATION NUMBER: 30-353
 ; REFERENCE/DOCKET NUMBER: 0656-048PC01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 251 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; PCT-US95-12357A-1

NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/861,464
 FILING DATE: 22-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/396, 001
 FILING DATE: 28-FEB-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/09351
 FILING DATE: 15-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/107, 408
 FILING DATE: 16-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: MTT-6408A2Z
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 508 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-861-464-10

RESULT ⁴
 US-08-396-001-10
 ; Sequence 10, Application US/08396001
 ; Patent No. 5919618
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarante, Leonard P.
 ; APPLICANT: Austruaco Jr., Nicancor
 ; APPLICANT: Claus, James
 ; APPLICANT: Cole, Francesca
 ; APPLICANT: Kennedy, Brian
 ; TITLE OF INVENTION: Genes Determining Cellular Senescence in
 ; YEAST
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk

RESULT ³
 US-08-861-464-10
 ; Sequence 10, Application US/08861464
 ; Patent No. 5874230
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarante, Leonard P.
 ; APPLICANT: Austruaco Jr., Nicancor
 ; APPLICANT: Kennedy, Brian
 ; TITLE OF INVENTION: Genes Determining Cellular Senescence
 ; in YEAST

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/396,001
 FILING DATE: 28-FEB-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 508 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-396-001-10

RESULT 5
 US-09-323-433A-10
 ; Sequence 10, Application US/09323433A
 ; Patent No. 6218512
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarante, Leonard P.
 ; APPLICANT: Ausriaco Jr., Nicanor
 ; APPLICANT: Claus, James J.
 ; APPLICANT: Cole, Francesca
 ; APPLICANT: Kennedy, Brian
 ; TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN YEAST
 ; FILE REFERENCE: 0050-1491-003
 ; CURRENT APPLICATION NUMBER: US/09/323,433A
 ; CURRENT FILING DATE: 1999-06-01
 ; PRIOR APPLICATION NUMBER: US 08/396,001
 ; PRIOR FILING DATE: 1995-02-28
 ; PRIOR APPLICATION NUMBER: PCT/US94/09351
 ; PRIOR FILING DATE: 1994-08-15
 ; PRIOR APPLICATION NUMBER: US 08/107,408
 ; PRIOR FILING DATE: 1993-08-16
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 508
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-323-433A-10

Query Match 73.8%; Score 31; DB 2; Length 508;
 Best Local Similarity 85.7%; Pred. No. 93; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0; 0; Gaps 0;
 Qy 2 LRDDLE 8
 Db 62 LRDDIVE 68

RESULT 6
 US-08-556-419-22

Query Match 73.8%; Score 31; DB 3; Length 508;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0; 0; Gaps 0;
 Qy 2 LRDDLE 8
 Db 62 LRDDIVE 68

RESULT 5
 US-08-556-419-23
 ; Sequence 23, Application US/08556419C
 ; Patent No. 6093549
 ; GENERAL INFORMATION:
 ; APPLICANT: Snyder, Solomon
 ; APPLICANT: Li, Xiao-Jiang
 ; APPLICANT: Li, Shi-Hua
 ; APPLICANT: Sharp, Alan
 ; APPLICANT: Granahan, Anthony
 ; APPLICANT: Worley, Paul
 ; APPLICANT: Snyder, Paul
 ; TITLE OF INVENTION: Huntingtin-associated protein
 ; FILE REFERENCE: 01107-52271
 ; CURRENT APPLICATION NUMBER: US/08/556,419C
 ; CURRENT FILING DATE: 1995-11-09
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 629
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-08-556-419-23

Query Match 73.8%; Score 31; DB 3; Length 629;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0; 0; Gaps 0;
 Qy 2 LRDDLE 8
 Db 205 LRDDLQ 211

RESULT 8
 US-08-469-005A-10
 ; Sequence 10, Application US/08469005A
 ; Patent No. 5663674
 ; GENERAL INFORMATION:
 ; APPLICANT: KUHADA, FRANCIS P.
 ; APPLICANT: PASTERNAK, GARY A.

TITLE OF INVENTION: CANCER RELATED ANTIGEN
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BAKER & BOTT'S, L.L.P.
 STREET: 1299 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20004-2400
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 CURRENT APPLICATION DATA:
 SOFTWARE: FASTSEQ Version 1.5
 APPLICATION NUMBER: US/08/469, 005A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION NUMBER: 08/188, 426
 APPLICATION NUMBER: 08/188, 426
 FILING DATE: 24-JAN-1994
 APPLICATION NUMBER: 08/036, 908
 FILING DATE: 26-JUL-1993
 APPLICATION NUMBER: 07/917, 716
 FILING DATE: 24-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: POSORSKE, Laurence H
 REGISTRATION NUMBER: 34, 698
 REFERENCE/DOCKET NUMBER: 062482-0113
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-639-7700
 TELEX: 202-639-7890
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2509 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US-08-469-005A-10

Query Match 73 8% Score 31; DB 1; Length 2509;
 Best Local Similarity 87.5%; Pred. No. 5.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDILLE 8
 Db 1972 VLRDGILE 1979

RESULT 9
 US-08-770-544-8
 Sequence 8, Application US/08770544
 Patent No. 5907085
 GENERAL INFORMATION:
 APPLICANT: Gonsalves, Dennis
 APPLICANT: Ling, Kai-Shu
 TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
 TITLE OF INVENTION: THEIR USES
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 STREET: Clinton Square, P.O. Box 1051
 CITY: Rochester
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 14603

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER:
 APPLICATION NUMBER: US/08/770, 544
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldblatt, Michael L.
 REGISTRATION NUMBER: 30,727
 REFERENCE/DOCKET NUMBER: 19603/621
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (716) 263-1304
 TELEFAX: (716) 263-1600
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 483 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-770-544-8

Query Match 71 4% Score 30; DB 2; Length 483;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDDLEA 9
 Db 124 RDDIMER 130

RESULT 10
 US-07-935-311A-4
 Sequence 4, Application US/07935311A
 Patent No. 5378809
 GENERAL INFORMATION:
 APPLICANT: Di Fiore, Pier Paolo
 APPLICANT: Fazioli, Francesca
 TITLE OF INVENTION: Substrate of the Epidermal Growth
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive, 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: USA
 ZIP: 92660

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/935, 311A
 FILING DATE: 199208/25
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelsen, Ned A.
 REGISTRATION NUMBER: 29, 655
 REFERENCE/DOCKET NUMBER: NHO35. 001A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-9550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:

LENGTH: 821 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-07-935-311A-4

Query Match 71.4%; Score 30; DB 1; Length 821;
 Best Local Similarity 62.5%; Pred. No. 2.5e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VRDLDLE 8
 Db 551 VMKDDVLE 558

RESULT 11
 US-08-368-079-4
 Sequence 4, Application US/08368079
 Patent No. 5610018

GENERAL INFORMATION:
 APPLICANT: Di Fiore, Pier Paolo
 APPLICANT: Fazio, Francesca
 TITLE OF INVENTION: egs8, A Substrate for the Epidermal Growth Factor
 TITLE OF INVENTION: Farnesate, Antibodies Thereto, and Methods of Use Thereof
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive, 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: USA
 ZIP: 92660

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FUSSEQ Version 1.5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/368,079
 FILING DATE: 03-JAN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/935,311
 FILING DATE: 25-AUG-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelson, Ned A.
 REGISTRATION NUMBER: 29, 655
 REFERENCE/DOCKET NUMBER: NIH035.001DV1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 821 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-368-079-4

Query Match 71.4%; Score 30; DB 1; Length 821;
 Best Local Similarity 62.5%; Pred. No. 2.5e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VRDLDLE 8
 Db 551 VMKDDVLE 558

RESULT 12
 US-09-489-07996-4
 Sequence 4, Application PC/TUSS9307996

Query Match 71.4%; Score 30; DB 2; Length 1159;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RDLDLE 8
 Db 835 RDLDLE 840

RESULT 14
 US-07-351-215-13
 Sequence 13, Application US/09351215

; Patent No. 6087488
 ; GENERAL INFORMATION:
 ; APPLICANT: Ganetzky, Barry S.
 ; TITLE: Titus, Steven A.
 ; TITLE OF INVENTION: Polynucleotides Encoding Herg-3
 ; FILE REFERENCE: 960296.94550
 ; CURRENT APPLICATION NUMBER: US/09/351,215
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: 08/956,242
 ; EARLIER FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 13
 ; LENGTH: 1159
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-351-215-13

Query Match 71.4%; Score 30; DB 3; Length 1159;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 RIDDLE 8
 Db 835 RIDDLE 840

RESULT 15
 US-09-222-012-2
 ; Sequence 2, Application US/09226012
 ; Patent No. 6207383
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating, Mark T.
 ; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
 ; TITLE OF INVENTION: SYNDROME GENE
 ; FILE REFERENCE: 233-136
 ; CURRENT APPLICATION NUMBER: US/09/226,012
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Query Match 71.4%; Score 30; DB 4; Length 1159;
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 QY 3 RIDDLE 8
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